Figure 1A

```
  1 CACCCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGC.AGCCC AAAGCTCCTC  60

 61 TGCCCACCCT GGCTCCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120

121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCCAGCAA 180

181 AGGCCTGAAG GAACAGGCCG GGAAGGAGC  CCTCCCTCTC TCCCTTGTCC CTCCATCCAC 240

241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
  1                              M   A   R   A   H   W   G   C   C   P   W   L   12

301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V   L   L   C   A   C   A   W   G   H   T   K   P   L   D   L   G   G   Q   D   32

361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V   R   N   C   S   T   N   P   P   Y   L   P   V   T   V   V   N   T   T   M   52

421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S   L   T   A   L   R   Q   Q   M   Q   T   Q   N   L   S   A   Y   I   I   P   72

481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCGTGGATT 540
 73 G   T   D   A   H   M   N   E   Y   I   G   Q   H   D   E   R   R   A   W   I   92

541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
 93 T   G   F   T   G   S   A   G   T   A   V   V   T   M   K   K   A   A   V   W   112

601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
113 T   D   S   R   Y   W   T   Q   A   E   R   Q   M   D   C   N   W   E   L   H   132

661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720
133 K   E   V   G   T   T   P   I   V   T   W   L   L   T   E   I   P   A   G   G   152

721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
153 R   V   G   F   D   P   F   L   L   S   I   D   T   W   E   S   Y   D   L   A   172

781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTGGA CCTGGTATGG 840
173 L   Q   G   S   N   R   Q   L   V   S   I   T   T   N   L   V   D   L   V   W   192

841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900
193 G   S   E   R   P   P   V   P   N   Q   P   I   Y   A   L   Q   E   A   F   T   212

901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
213 G   S   T   W   Q   E   K   V   S   G   V   R   S   Q   M   Q   K   H   Q   K   232
```

Figure 1B

```
 961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V  P  T  A   V  L  L    S  A  L    E  E  T    A  W  L    F  N  L  R  252


1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
 253 A  S  D  I   P  Y  N    P  F  F    Y  S  Y  T   L  L  T    D  S  S   272


1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACTCC 1140
 273 I  R  L  F   A  N  K    S  R  F    S  S  E  T   L  S  Y    L  N  S   292


1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S  C  T  G   P  M  C    V  Q  I    E  D  Y    S  Q  V  R   D  S  I   312


1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q  A  Y  S   L  G  D    V  R  I    W  I  G  T   S  Y  T    M  Y  G   332


1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I  Y  E  M   I  P  R    E  K  L    V  T  D  T   Y  S  P    V  M  M   352


1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
 353 T  K  A  V   K  N  S    K  E  Q    A  L  L    K  A  S  H   V  R  D   372


1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
 373 A  V  A  V   I  R  Y    L  V  W    L  E  K    N  V  P  K   G  T  V   392


1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
 393 D  E  F  S   G  A  E    I  V  D    K  F  R  G   E  E  Q    F  S  S   412


1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
 413 G  P  S  F   E  T  I    S  A  S    G  L  N    A  A  L  A   H  Y  S   432


1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P  T  K  E   L  N  R    K  L  S    S  D  E  M   Y  L  L    D  S  G   452


1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
 453 G  Q  Y  W   D  G  T    T  D  I    T  R  T  V   H  W  G    T  P  S   472


1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A  F  Q  K   E  A  Y    T  R  V    L  I  G  N   I  D  L    S  R  L   492


1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
 493 I  F  P  A   A  T  S    G  R  M    V  E  A  F   A  R  R    A  L  W   512


1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
 513 D  A  G  L   N  Y  G    H  G  T    G  H  G  I   G  N  F    L  C  V   532
```

Figure 1C

```
1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H   E   W   P   V   G   F   Q   S   N   N   I   A   M   A   K   G   M   F   T  552


1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S   I   E   P   G   Y   Y   K   D   G   E   F   G   I   R   L   E   D   V   A  572


1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L   V   V   E   A   K   T   K   Y   P   G   E   L   P   D   L   V   V   S   F  592


2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCGAGCA TCTCCAGTAC 2100
 593 V   P   Y   D   R   N   L   I   D   V   S   L   L   S   P   E   H   L   Q   Y  612


2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC AGAGCTGCA GAGGCGCCAG 2160
 613 L   N   R   Y   Y   Q   T   I   R   E   K   V   G   P   E   L   Q   R   R   Q  632


2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L   L   E   E   F   E   W   L   Q   Q   H   T   E   P   L   A   A   R   A   P  652


2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D   T   A   S   W   A   S   V   L   V   V   S   T   L   A   I   L   G   W   S  672


2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V   *                                                                        673


2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400


2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460


2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520


2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580


2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640


2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700


2701 CCTGTCACCG CGTGTTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760


2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820


2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880


2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940
```

Figure 1D

```
2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000

3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTC GAGGAGCCCT TTGAACTTTC 3060

3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCCTTC 3120

3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAACTG AGCTTCAGAC 3180

3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240

3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300

3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360

3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420

3421 GCCTGTGG 3428
```

Figure 2A

```
  1 CACCCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC  60


 61 TGCCCACCCT GGCTCCCAAA ACCCTCCAAA ACAAAGACC  AGAAAAGCAC TCTCCACCCA 120


121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCCAGGAA 180


181 AGGCCTGAAG GAACAGGCCG GGGAAGGAGC CCTCCCTCTC TCCCTTGTCC CTCCATCCAC 240


241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
  1                      M   A   R   H   W   G   C   C   P   W   L    12


301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V   L   L   C   A   C   A   W   G   H   T   K   P   L   D   L   G   G   Q   D   32


361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V   R   N   C   S   T   N   P   P   Y   L   P   V   T   V   V   N   T   T   M   52


421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S   L   T   A   L   R   Q   Q   M   Q   T   Q   N   L   S   A   Y   I   I   P   72


481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCGTGGATT 540
 73 G   T   D   A   H   M   N   E   Y   I   G   Q   H   D   E   R   R   A   W   I   92


541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
 93 T   G   F   T   G   S   A   G   T   A   V   V   T   M   K   K   A   A   V   W   112


601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
113 T   D   S   R   Y   W   T   Q   A   E   R   Q   M   D   C   N   W   E   L   H   132


661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720
133 K   E   V   G   T   T   P   I   V   T   W   L   L   T   E   I   P   A   G   G   152


721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
153 R   V   G   F   D   P   F   L   L   S   I   D   T   W   E   S   Y   D   L   A   172


781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTGGA CCTGGTATGG 840
173 L   Q   G   S   N   R   Q   L   V   S   I   T   T   N   L   V   D   L   V   W   192


841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900
193 G   S   E   R   P   P   V   P   N   Q   P   I   Y   A   L   Q   E   A   F   T   212


901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
213 G   S   T   W   Q   E   K   V   S   G   V   R   S   Q   M   Q   K   H   Q   K   232
```

Figure 2B

```
 961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V   P   T   A   V   L   L   S   A   L   E   E   T   A   W   L   F   N   L   R   252


1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
 253 A   S   D   I   P   Y   N   P   F   F   Y   S   Y   T   L   L   T   D   S   S· 272


1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACTCC 1140
 273 I   R   L   F   A   N   K   S   R   F   S   S   E   T   L   S   Y   L   N   S   292


1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S   C   T   G   P   M   C   V   Q   I   E   D   Y   S   Q   V   R   D   S   I   312


1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q   A   Y   S   L   G   D   V   R   I   W   I   G   T   S   Y   T   M   Y   G   332


1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I   Y   E   M   I   P   R   E   K   L   V   T   D   T   Y   S   P   V   M   M   352


1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
 353 T   K   A   V   K   N   S   K   E   Q   A   L   L   K   A   S   H   V   R   D   372


1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
 373 A   V   A   V   I   R   Y   L   V   W   L   E   K   N   V   P   K   G   T   V   392


1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
 393 D   E   F   S   G   A   E   I   V   D   K   F   R   G   E   E   Q   F   S   S   412


1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
 413 G   P   S   F   E   T   I   S   A   S   G   L   N   A   A   L   A   H   Y   S   432


1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P   T   K   E   L   N   R   K   L   S   S   D   E   M   Y   L   L   D   S   G   452


1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
 453 G   Q   Y   W   D   G   T   T   D   I   T   R   T   V   H   W   G   T   P   S   472


1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A   F   Q   K   E   A   Y   T   R   V   L   I   G   N   I   D   L   S   R   L   492


1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
 493 I   F   P   A   A   T   S   G   R   M   V   E   A   F   A   R   R   A   L   W   512


1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
 513 D   A   G   L   N   Y   G   H   G   T   G   H   G   I   G   N   F   L   C   V   532
```

Figure 2C

```
1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H    E   W   P    V   G   F    Q   S   N    N   I   A    M   A   K   G    M   F   T   552


1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S    I   E   P    G   Y   Y    K   D   G    E   F   G    I   R   L   E    D   V   A   572


1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L    V   V   E    A   K   T    K   Y   P    G   E   L    P   D   L   V    V   S   F   592


2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCGGAGCA TCTCCAGTAC 2100
 593 V    P   Y   D    R   N   L    I   D   V    S   L   L    S   P   E   H    L   Q   Y   612


2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L    N   R   Y    Y   Q   T    I   R   E    K   V   G    P   E   L   Q    R   R   Q   632


2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L    L   E   E    F   E   W    L   Q   Q    H   T   E    P   L   A   A    R   A   P   652


2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D    T   A   S    W   A   S    V   L   V    V   S   T    L   A   I   L    G   W   S   672


2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V    *                                                                    673


2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400


2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460


2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520


2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580


2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640


2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG AAAACCCAA 2700


2701 CCTGTCACCG CGTGTTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760


2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820


2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880


2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940
```

Figure 2D

```
2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000

3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTC GAGGAGCCCT TTGAACTTTC 3060

3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCCTTC 3120

3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAACTG AGCTTCAGAC 3180

3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240

3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300

3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360

3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420

3421 GCCTGTGG 3428
```

Figure 3A

```
  1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC  60
  1     M    A    S    S    W    P    P    L    E    L    Q    S    S    N    Q    S    Q    L   18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19    F    P    Q    N    A    T    A    C    D    N    A    P    E    A    W    D    L    L    H    R   38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39    V    L    P    T    F    I    I    S    I    C    F    F    G    L    L    G    N    L    F    V   58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59    L    L    V    F    L    L    P    R    R    Q    L    N    V    A    E    I    Y    L    A    N   78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT CTGGGCAGA GAATATCTGG 300
 79    L    A    A    S    D    L    V    F    V    L    G    L    P    F    W    A    E    N    I    W   98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99    N    Q    F    N    W    P    F    G    A    L    L    C    R    V    I    N    G    V    I    K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119    A    N    L    F    I    S    I    F    L    V    V    A    I    S    Q    D    R    Y    R    V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139    L    V    H    P    M    A    S    G    R    Q    Q    R    R    R    Q    A    R    V    T    C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159    V    L    I    W    V    V    G    G    L    L    S    I    P    T    F    L    L    R    S    I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179    Q    A    V    P    D    L    N    I    T    A    C    I    L    L    L    P    H    E    A    W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199    H    F    A    R    I    V    E    L    N    I    L    G    F    L    L    P    L    A    A    I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219    V    F    F    N    Y    H    I    L    A    S    L    R    T    R    E    E    V    S    R    T  238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239    R    V    R    G    P    K    D    S    K    T    T    A    L    I    L    T    L    V    V    A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259    F    L    V    C    W    A    P    Y    H    F    F    A    F    L    E    F    L    F    Q    V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279    Q    A    V    R    G    C    F    W    E    D    F    I    D    L    G    L    Q    L    A    N  298
```

Figure 3B

```
901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F   F   A   F   T   N   S    S   L   N    P   V   I   Y    V   F   V    G   R   L   318


961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F   R   T   K    V   W   E    L   Y   K    Q   C   T   P    K   S   L    A   P   I   338


1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S   S   S   H    R   K   E    I   F   Q    L   F   W   R    N   *   353
```

1081 CC 1082

Figure 4A

```
  1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
  1     M   A   S   S   W   P   P   L   E   L   Q   S   S   N   Q   S   Q   L  18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F   P   Q   N   A   T   A   C   D   N   A   P   E   A   W   D   L   L   H   R  38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39 V   L   P   T   F   I   I   S   I   C   F   F   G   L   L   G   N   L   F   V  58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L   L   V   F   L   L   P   R   R   Q   L   N   V   A   E   I   Y   L   A   N  78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L   A   A   S   D   L   V   F   V   L   G   L   P   F   W   A   E   N   I   W  98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N   Q   F   N   W   P   F   G   A   L   L   C   R   V   I   N   G   V   I   K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A   N   L   F   I   S   I   F   L   V   V   A   I   S   Q   D   R   Y   R   V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139 L   V   H   P   M   A   S   G   R   Q   Q   R   R   R   Q   A   R   V   T   C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V   L   I   W   V   V   G   G   L   L   S   I   P   T   F   L   L   R   S   I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q   A   V   P   D   L   N   I   T   A   C   I   L   L   L   P   H   E   A   W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H   F   A   R   I   V   E   L   N   I   L   G   F   L   L   P   L   A   A   I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V   F   F   N   Y   H   I   L   A   S   L   R   T   R   E   E   V   S   R   T  238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R   V   R   G   P   K   D   S   K   T   T   A   L   I   L   T   L   V   V   A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F   L   V   C   W   A   P   Y   H   F   F   A   F   L   E   F   L   F   Q   V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q   A   V   R   G   C   F   W   E   D   F   I   D   L   G   L   Q   L   A   N  298
```

Figure 4B

```
  901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCAGCTC  960
  299 F    F    A    F    T    N    S    S    L    N    P    V    I    Y    V    F    V    G    Q    L    318


  961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
  319 F    R    T    K    V    W    E    L    Y    K    Q    C    T    P    K    S    L    A    P    I    338


 1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
  339 S    S    S    H    R    K    E    I    F    Q    L    F    W    R    N    *                     353


 1081 CC 1082
```

Figure 5A

```
  1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC  60
  1         M   S   S   W   P   P   L   E   L   Q   S   S   N   Q   S   Q   L  18


 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F   P   Q   N   A   T   A   C   D   N   A   P   E   A   W   D   L   L   H   R  38


121 GTGCTGCCAA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39 V   L   P   T   F   I   I   S   I   C   F   F   G   L   L   G   N   L   F   V  58


181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L   L   V   F   L   L   P   R   R   Q   L   N   V   A   E   I   Y   L   A   N  78


241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L   A   A   S   D   L   V   F   V   L   G   L   P   F   W   A   E   N   I   W  98


301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N   Q   F   N   W   P   F   G   A   L   L   C   R   V   I   N   G   V   I   K 118


361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A   N   L   F   I   S   I   F   L   V   V   A   I   S   Q   D   R   Y   R   V 138


421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139 L   V   H   P   M   A   S   G   R   Q   Q   R   R   Q   A   R   V   T   C 158


481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V   L   I   W   V   V   G   G   L   L   S   I   P   T   F   L   L   R   S   I 178


541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q   A   V   P   D   L   N   I   T   A   C   I   L   L   L   P   H   E   A   W 198


601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H   F   A   R   I   V   E   L   N   I   L   G   F   L   L   P   L   A   A   I 218


661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V   F   F   N   Y   H   I   L   A   S   L   R   T   R   E   E   V   S   R   T 238


721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R   V   R   G   P   K   D   S   K   T   T   A   L   I   L   T   L   V   V   A 258


781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F   L   V   C   W   A   P   Y   H   F   F   A   F   L   E   F   L   F   Q   V 278


841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q   A   V   R   G   C   F   W   E   D   F   I   D   L   G   L   Q   L   A   N 298
```

Figure 5B

```
901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F    F   A   F     T   N   S     S   L   N     P   V   I   Y     V   F   V     G   R   L   318


961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F    R   T   K     V   W   E     L   Y   K     Q   C   T   P     K   S   L     A   P   I   338


1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S    S   S   H     R   K   E     I   F   Q     L   F   W   R     N   *                    353


1081 CC 1082
```

Figure 6A

```
  1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACC  60
  1 M   F   S   P   W   K   I   S   M   F   L   S   V   R   E   D   S   V   P   T    20

 61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
 21 T   A   S   F   S   A   D   M   L   N   V   T   L   Q   G   P   T   L   N   G    40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T   F   A   Q   S   K   C   P   Q   V   E   W   L   G   W   L   N   T   I   Q    60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
 61 P   P   F   L   W   V   L   F   V   L   A   T   L   E   N   I   F   V   L   S    80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V   F   C   L   H   K   S   S   C   T   V   A   E   I   Y   L   G   N   L   A   100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A   A   D   L   I   L   A   C   G   L   P   F   W   A   I   T   I   S   N   N   120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F   D   W   L   F   G   E   T   L   C   R   V   V   N   A   I   I   S   M   N   140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L   Y   S   S   I   C   F   L   M   L   V   S   I   D   R   Y   L   A   L   V   160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K   T   M   S   M   G   R   M   R   G   V   R   W   A   K   L   Y   S   L   V   180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
181 I   W   G   C   T   L   L   L   S   S   P   M   L   V   F   R   T   M   K   E   200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y   S   D   E   G   H   N   V   T   A   C   V   I   S   Y   P   S   L   I   W   220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E   V   F   T   N   M   L   L   N   V   V   G   F   L   L   P   L   S   V   I   240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T   F   C   T   M   Q   I   M   Q   V   L   R   N   N   E   M   Q   K   F   K   260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E   I   Q   T   E   R   R   A   T   V   L   V   L   V   V   L   L   F   I   280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I   C   W   L   P   F   Q   I   S   T   F   L   D   T   L   H   R   L   G   I   300
```

Figure 6B

```
 901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG  960
 301 L    S    S    Q    D    E    R    I    I    D    V    I    T    Q    I    A    S    F    M    320

 961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A    Y    S    N    S    C    L    N    P    L    V    Y    V    I    V    G    K    R    F    R    340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K    K    S    W    E    V    Y    Q    G    V    C    Q    K    G    G    C    R    S    E    P    360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I    Q    M    E    N    S    M    G    T    L    R    T    S    I    S    V    E    R    Q    I    380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H    K    L    Q    D    W    A    G    S    R    Q    *                                391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040
```

Figure 6C

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2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100

2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160

2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220

2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280

2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340

2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400

2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460

2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520

2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580

2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640

2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700

2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760

2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820

2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880

2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940

2941 GAGGGCTAGA ACCTAGAAGG CTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000

3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060

3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120

3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180

3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTTAAA GCAAAGCGT GAAAAAAAAG 3240
```

Figure 6D

```
3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAAA AAA 3733
```

Figure 7A

```
  1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60


 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120


121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180


181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
  1                                         M   D   N   V   L   P   V   D   S   D  10


241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L   S   P   N   I   S   T   N   T   S   E   P   N   Q   F   V   Q   P   A   W  30


301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q   I   V   L   W   A   A   A   Y   T   V   I   V   V   T   S   V   V   G   N  50


361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V   V   V   M   W   I   I   L   A   H   K   R   M   R   T   V   T   N   Y   F  70


421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L   V   N   L   A   F   A   E   A   S   M   A   A   F   N   T   V   V   N   F  90


481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540
 91 T   Y   A   V   H   N   E   W   Y   Y   G   L   F   Y   C   K   F   H   N   F  110


541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
111 F   P   I   A   V   F   A   S   I   Y   S   M   T   A   V   A   F   D   R  130


601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
131 Y   M   A   I   I   H   P   L   Q   P   R   L   S   A   T   A   T   K   V   V  150


661 ATCTGTGTCA TCTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
151 I   C   V   I   W   V   L   A   L   L   L   A   F   P   Q   G   Y   Y   S   T  170


721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
171 T   E   T   M   P   S   R   V   V   C   M   I   E   W   P   E   H   P   N   K  190


781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
191 I   Y   E   K   V   Y   H   I   C   V   T   V   L   I   Y   F   L   P   L   L  210


841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
211 V   I   G   Y   A   Y   T   V   V   G   I   T   L   W   A   S   E   I   P   G  230


901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
231 D   S   S   D   R   Y   H   E   Q   V   S   A   K   R   K   V   V   K   M   M  250
```

Figure 7B

```
 961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCTCCTG 1020
 251 I   V   V   C   T   F   A   I   C   W   L   P   F   H   I   F   F   L   L   270


1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P   Y   I   N   P   D   L   Y   L   K   K   F   I   Q   Q   V   Y   L   A   I   290


1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M   W   L   A   M   S   S   T   M   Y   N   P   I   I   Y   C   C   L   N   D   310


1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R   F   R   L   G   F   K   H   A   F   R   C   C   P   F   I   S   A   G   D   330


1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y   E   G   L   E   M   K   S   T   R   Y   L   Q   T   Q   G   S   V   Y   K   350


1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V   S   R   L   E   T   T   I   S   T   V   V   G   A   H   E   E   E   P   E   370


1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D   G   P   K   A   T   P   S   S   L   D   L   T   S   N   C   S   S   R   S   390


1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D   S   K   T   M   T   E   S   F   S   F   S   S   N   V   L   S   *       407


1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500


1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560


1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620


1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680


1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740


1741 TGCATGCGAG TGCTCATTTC AGGATG 1766
```

Figure 8A

```
  1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60


 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120


121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180


181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
  1                                  M   D   N   V   L   P   V   D   S   D  10


241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L   S   P   N   I   S   T   N   T   S   E   P   N   Q   F   V   Q   P   A   W  30


301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q   I   V   L   W   A   A   A   Y   T   V   I   V   V   T   S   V   V   G   N  50


361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V   V   V   M   W   I   I   L   A   H   K   R   M   R   T   V   T   N   Y   F  70


421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT CAATACAGT GGTGAACTTC 480
 71 L   V   N   L   A   F   A   E   A   S   M   A   A   F   N   T   V   V   N   F  90


481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540
 91 T   Y   A   V   H   N   E   W   Y   Y   G   L   F   Y   C   K   F   H   N   F  110


541 TTCCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
111 F   P   I   A   V   F   A   S   I   Y   S   M   T   A   V   A   F   D   R  130


601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
131 Y   M   A   I   I   H   P   L   Q   P   R   L   S   A   T   A   T   K   V   V  150


661 ATCTGTGTCA TCTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCAGGGCTA CTACTCAACC 720
151 I   C   V   I   W   V   L   A   L   L   L   A   F   P   Q   G   Y   Y   S   T  170


721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
171 T   E   T   M   P   S   R   V   V   C   M   I   E   W   P   E   H   P   N   K  190


781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
191 I   Y   E   K   V   Y   H   I   C   V   T   V   L   I   Y   F   L   P   L   L  210


841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
211 V   I   G   Y   A   Y   T   V   V   G   I   T   L   W   A   S   E   I   P   G  230


901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
231 D   S   S   D   R   Y   H   E   Q   V   S   A   K   R   K   V   V   K   M   M  250
```

Figure 8B

```
 961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCTCCTG 1020
 251 I  V  V  V   C  T  F   A  I  C   W  L  P  F   H  I  F   F  L  L   270


1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P  Y  I  N   P  D  L   Y  L  K   K  F  I  Q   Q  V  Y   L  A  I   290


1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M  W  L  A   M  S  S   T  M  Y   N  P  I  I   Y  C  C   L  N  D   310


1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R  F  R  L   G  F  K   H  A  F   R  C  C  P   F  I  S   A  G  D   330


1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y  E  G  L   E  M  K   S  T  R   Y  L  Q  T   Q  G  S   V  Y  K   350


1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V  S  R  L   E  T  T   I  S  T   V  V  G  A   H  E  E   E  P  E   370


1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D  G  P  K   A  T  P   S  S  L   D  L  T  S   N  C  S   S  R  S   390


1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D  S  K  T   M  T  E   S  F  S   F  S  S  N   V  L  S   *         407


1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500


1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560


1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620


1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680


1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740


1741 TGCATGCGAG TGCTCATTTC AGGATG 1766
```

Figure 9A

```
  1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60


 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120


121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180


181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
  1                                  M  D  N  V  L  P  V  D  S  D  10


241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L  S  P  N  I  S  T  N  T  S  E  P  N  Q  F  V  Q  P  A  W  30


301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q  I  V  L  W  A  A  A  Y  T  V  I  V  V  T  S  V  V  G  N  50


361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V  V  V  M  W  I  I  L  A  H  K  R  M  R  T  V  T  N  Y  F  70


421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L  V  N  L  A  F  A  E  A  S  M  A  A  F  N  T  V  V  N  F  90


481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540
 91 T  Y  A  V  H  N  E  W  Y  Y  G  L  F  Y  C  K  F  H  N  F  110


541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
111 F  P  I  A  A  V  F  A  S  I  Y  S  M  T  A  V  A  F  D  R  130


601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
131 Y  M  A  I  I  H  P  L  Q  P  R  L  S  A  T  A  T  K  V  V  150


661 ATCTGTGTCA TATGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
151 I  C  V  I  W  V  L  A  L  L  L  A  F  P  Q  G  Y  Y  S  T  170


721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
171 T  E  T  M  P  S  R  V  V  C  M  I  E  W  P  E  H  P  N  K  190


781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
191 I  Y  E  K  V  Y  H  I  C  V  T  V  L  I  Y  F  L  P  L  L  210


841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
211 V  I  G  Y  A  Y  T  V  V  G  I  T  L  W  A  S  E  I  P  G  230


901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
231 D  S  S  D  R  Y  H  E  Q  V  S  A  K  R  K  V  V  K  M  M  250
```

Figure 9B

```
 961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCTCCTG 1020
 251 I  V  V  V   C  T  F   A  I  C   W  L  P   F  H  I  F   F  L  L   270


1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P  Y  I  N   P  D  L   Y  L  K   K  F  I  Q   Q  V  Y   L  A  I   290


1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M  W  L  A   M  S  S   T  M  Y   N  P  I  I   Y  C  C   L  N  D   310


1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R  F  R  L   G  F  K   H  A  F   R  C  C  P   F  I  S   A  G  D   330


1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y  E  G  L   E  M  K   S  T  R   Y  L  Q  T   Q  G  S   V  Y  K   350


1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V  S  R  L   E  T  T   I  S  T   V  V  G  A   H  E  E   E  P  E   370


1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D  G  P  K   A  T  P   S  S  L   D  L  T  S   N  C  S   S  R  S   390


1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D  S  K  T   M  T  E   S  F  S   F  S  S  N   V  L  S   *          407


1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500


1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560


1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620


1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680


1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740


1741 TGCATGCGAG TGCTCATTTC AGGATG 1766
```

Figure 10A

```
  1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC  60

 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120

121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180

181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
  1                                       M   D   N   V   L   P   V   D   S   D  10

241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L   S   P   N   I   S   T   N   T   S   E   P   N   Q   F   V   Q   P   A   W  30

301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q   I   V   L   W   A   A   A   Y   T   V   I   V   V   T   S   V   V   G   N  50

361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V   V   V   M   W   I   I   L   A   H   K   R   M   R   T   V   T   N   Y   F  70

421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L   V   N   L   A   F   A   E   A   S   M   A   A   F   N   T   V   V   N   F  90

481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540
 91 T   Y   A   V   H   N   E   W   Y   Y   G   L   F   Y   C   K   F   H   N   F 110

541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
111 F   P   I   A   A   V   F   A   S   I   Y   S   M   T   A   V   A   F   D   R 130

601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
131 Y   M   A   I   I   H   P   L   Q   P   R   L   S   A   T   A   T   K   V   V 150

661 ATCTGTGTCA TCTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
151 I   C   V   I   W   V   L   A   L   L   L   A   F   P   Q   G   Y   Y   S   T 170

721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
171 T   E   T   M   P   S   R   V   V   C   M   I   E   W   P   E   H   P   N   K 190

781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
191 I   Y   E   K   V   Y   H   I   C   V   T   V   L   I   Y   F   L   P   L   L 210

841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
211 V   I   G   Y   A   Y   T   V   V   G   I   T   L   W   A   S   E   I   P   G 230

901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
231 D   S   S   D   R   Y   H   E   Q   V   S   A   K   R   K   V   V   K   M   M 250
```

Figure 10B

```
 961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCTCCTG 1020
 251 I   V   V   V   C   T   F   A   I   C   W   L   P   F   H   I   F   F   L   L   270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P   Y   I   N   P   D   L   Y   L   K   K   F   I   Q   Q   V   Y   L   A   I   290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M   W   L   A   M   S   S   T   M   Y   N   P   I   I   Y   C   C   L   N   D   310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R   F   R   L   G   F   K   H   A   F   R   C   C   P   F   I   S   A   G   D   330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y   E   G   L   E   M   K   S   T   R   Y   L   Q   T   Q   G   S   V   Y   K   350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V   S   R   L   E   T   T   I   S   T   V   V   G   A   H   E   E   E   P   E   370

1321 GACGGCCCCA AGGCCACACC CTCATCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D   G   P   K   A   T   P   S   S   L   D   L   T   S   N   C   S   S   R   S   390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D   S   K   T   M   T   E   S   F   S   F   S   S   N   V   L   S   *   407

1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766
```

Figure 11A

```
  1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCCAG  60


 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
  1 M   A   S   R   L   T   L   L   T   L   L   L   L   L   A   G   D   R   A    20


121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S   S   N   P   N   A   T   S   S   S   Q   D   P   E   S   L   Q   D   R    40


181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G   E   G   K   V   A   T   T   V   I   S   K   M   L   F   V   E   P   I   L    60


241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E   V   S   L   P   T   T   N   S   T   T   N   S   A   T   K   I   T   A    80


301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N   T   T   D   E   P   T   T   Q   P   T   T   E   P   T   T   Q   P   T   I   100


361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q   P   T   Q   P   T   T   Q   L   P   T   D   S   P   T   Q   P   T   T   G   120


421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S   F   C   P   G   P   V   T   L   C   S   D   L   E   S   H   S   T   E   A   140


481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V   L   G   D   A   L   V   D   F   S   L   K   L   Y   H   A   F   S   A   M   160


541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K   K   V   E   T   N   M   A   F   S   P   F   S   I   A   S   L   L   T   Q   180


601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V   L   L   G   A   G   Q   N   T   K   T   N   L   E   S   I   L   S   Y   P   200


661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K   D   F   T   C   V   H   Q   A   L   K   G   F   T   T   K   G   V   T   S   220


721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V   S   Q   I   F   H   S   P   D   L   A   I   R   D   T   F   V   N   A   S   240


781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R   T   L   Y   S   S   S   P   R   V   L   S   N   N   S   D   A   N   L   E   260


841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L   I   N   T   W   V   A   K   N   T   N   N   K   I   S   R   L   L   D   S   280


901 CTGCCCTCCG ATACCCGCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L   P   S   D   T   R   L   V   L   L   N   A   I   Y   L   S   A   K   W   K   300
```

Figure 11B

```
 961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T   T   F   D   P   K   K   T   R   M   E   P  F   H   F   K   N   S   V   I   320


1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTTG 1080
 321 K   V   P   M   M   N   S   K   K   Y   P   V   A   H   F   I   D   Q   T   L   340


1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K   A   K   V   G   Q   L   Q   L   S   H   N   L   S   L   V   I   L   V   P   360


1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q   N   L   K   H   R   L   E   D   M   E   Q   A   L   S   P   S   V   F   K   380


1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A   I   M   E   K   L   E   M   S   K   F   Q   P   T   L   L   T   L   P   R   400


1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I   K   V   T   T   S   Q   D   M   L   S   I   M   E   K   L   E   F   F   D   420


1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
 421 F   S   Y   D   L   N   L   C   G   L   T   E   D   P   D   L   Q   V   S   A   440


1381 ATGCAGCACC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M   Q   H   Q   T   V   L   E   L   T   E   T   G   V   E   A   A   A   S   460


1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A   I   S   V   A   R   T   L   L   V   F   E   V   Q   Q   P   F   L   F   V   480


1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L   W   D   Q   Q   H   K   F   P   V   F   M   G   R   V   Y   D   P   R   A   500


1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620


1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680


1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740


1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800


1801 TCTATAAATA AAACCTGACA GACCAT 1826
```

Figure 12A

```
  1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCCAG  60


 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
  1 M   A   S   R   L   T   L   L   T   L   L   L   L   L   A   G   D   R   A   20


121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S   S   N   P   N   A   T   S   S   S   Q   D   P   E   S   L   Q   D   R   40


181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G   E   G   K   V   A   T   T   V   I   S   K   M   L   F   V   E   P   I   L   60


241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E   V   S   S   L   P   T   T   N   S   T   T   N   S   A   T   K   I   T   A   80


301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N   T   T   D   E   P   T   T   Q   P   T   T   E   P   T   T   Q   P   T   I  100


361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q   P   T   Q   P   T   T   Q   L   P   T   D   S   P   T   Q   P   T   T   G  120


421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S   F   C   P   G   P   V   T   L   C   S   D   L   E   S   H   S   T   E   A  140


481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V   L   G   D   A   L   V   D   F   S   L   K   L   Y   H   A   F   S   A   M  160


541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K   K   V   E   T   N   M   A   F   S   P   F   S   I   A   S   L   L   T   Q  180


601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V   L   L   G   A   G   Q   N   T   K   T   N   L   E   S   I   L   S   Y   P  200


661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K   D   F   T   C   V   H   Q   A   L   K   G   F   T   T   K   G   V   T   S  220


721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V   S   Q   I   F   H   S   P   D   L   A   I   R   D   T   F   V   N   A   S  240


781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R   T   L   Y   S   S   S   P   R   V   L   S   N   N   S   D   A   N   L   E  260


841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L   I   N   T   W   V   A   K   N   T   N   N   K   I   S   R   L   L   D   S  280


901 CTGCCCTCCG ATACCCGCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L   P   S   D   T   R   L   V   L   L   N   A   I   Y   L   S   A   K   W   K  300
```

Figure 12B

```
 961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T   T   F   D   P   K   K   T   R   M   E   P   F   H   F   K   N   S   V   I   320


1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTTG 1080
 321 K   V   P   M   M   N   S   K   K   Y   P   V   A   H   F   I   D   Q   T   L   340


1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K   A   K   V   G   Q   L   Q   L   S   H   N   L   S   L   V   I   L   V   P   360


1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q   N   L   K   H   R   L   E   D   M   E   Q   A   L   S   P   S   V   F   K   380


1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A   I   M   E   K   L   E   M   S   K   F   Q   P   T   L   L   T   L   P   R   400


1261 ATCAAAGTGA CGACCAGTCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I   K   V   T   T   S   Q   D   M   L   S   I   M   E   K   L   E   F   F   D   420


1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
 421 F   S   Y   D   L   N   L   C   G   L   T   E   D   P   D   L   Q   V   S   A   440


1381 ATGCAGCACC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M   Q   H   Q   T   V   L   E   L   T   E   T   G   V   E   A   A   A   A   S   460


1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A   I   S   V   A   R   T   L   L   V   F   E   V   Q   Q   P   F   L   F   V   480


1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L   W   D   Q   Q   H   K   F   P   V   F   M   G   R   V   Y   D   P   R   A   500


1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620


1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680


1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740


1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800


1801 TCTATAAATA AAACCTGACA GACCAT 1826
```

Figure 13A

```
  1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCCAG 60


 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
  1 M   A   S   R   L   T   L   L   T   L   L   L   L   L   A   G   D   R   A   20


121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S   S   N   P   N   A   T   S   S   S   Q   D   P   E   S   L   Q   D   R   40


181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGCTGA ACCCATCCTG 240
 41 G   E   G   K   V   A   T   T   V   I   S   K   M   L   F   A   E   P   I   L   60


241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E   V   S   S   L   P   T   T   N   S   T   T   N   S   A   T   K   I   T   A   80


301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N   T   T   D   E   P   T   Q   P   T   T   E   P   T   T   Q   P   T   I   100


361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q   P   T   Q   P   T   T   Q   L   P   T   D   S   P   T   Q   P   T   T   G   120


421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S   F   C   P   G   P   V   T   L   C   S   D   L   E   S   H   S   T   E   A   140


481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V   L   G   D   A   L   V   D   F   S   L   K   L   Y   H   A   F   S   A   M   160


541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K   K   V   E   T   N   M   A   F   S   P   F   S   I   A   S   L   L   T   Q   180


601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V   L   L   G   A   G   Q   N   T   K   T   N   L   E   S   I   L   S   Y   P   200


661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K   D   F   T   C   V   H   Q   A   L   K   G   F   T   T   K   G   V   T   S   220


721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V   S   Q   I   F   H   S   P   D   L   A   I   R   D   T   F   V   N   A   S   240


781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R   T   L   Y   S   S   S   P   R   V   L   S   N   N   S   D   A   N   L   E   260


841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L   I   N   T   W   V   A   K   N   T   N   N   K   I   S   R   L   L   D   S   280


901 CTGCCCTCCG ATACCCGCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L   P   S   D   T   R   L   V   L   L   N   A   I   Y   L   S   A   K   W   K   300
```

Figure 13B

```
 961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T   T   F   D   P   K   K   T   R   M   E   P   F   H   F   K   N   S   V   I  320


1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTTG 1080
 321 K   V   P   M   M   N   S   K   K   Y   P   V   A   H   F   I   D   Q   T   L  340


1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K   A   K   V   G   Q   L   Q   L   S   H   N   L   S   L   V   I   L   V   P  360


1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q   N   L   K   H   R   L   E   D   M   E   Q   A   L   S   P   S   V   F   K  380


1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A   I   M   E   K   L   E   M   S   K   F   Q   P   T   L   L   T   L   P   R  400


1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I   K   V   T   T   S   Q   D   M   L   S   I   M   E   K   L   E   F   F   D  420


1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
 421 F   S   Y   D   L   N   L   C   G   L   T   E   D   P   D   L   Q   V   S   A  440


1381 ATGCAGCACC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M   Q   H   Q   T   V   L   E   L   T   E   T   G   V   E   A   A   A   A   S  460


1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A   I   S   V   A   R   T   L   L   V   F   E   V   Q   Q   P   F   L   F   V  480


1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L   W   D   Q   Q   H   K   F   P   V   F   M   G   R   V   Y   D   P   R   A  500


1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620


1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680


1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740


1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800


1801 TCTATAAATA AAACCTGACA GACCAT 1826
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Figure 14A

```
  1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCCAG  60


 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
  1 M   A   S   R   L   T   L   L   T   L   L   L   L   L   A   G   D   R   A    20


121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S   S   N   P   N   A   T   S   S   S   S   Q   D   P   E   S   L   Q   D   R    40


181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G   E   G   K   V   A   T   T   V   I   S   K   M   L   F   V   E   P   I   L    60


241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E   V   S   S   L   P   T   T   N   S   T   T   N   S   A   T   K   I   T   A    80


301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N   T   T   D   E   P   T   T   Q   P   T   T   E   P   T   T   Q   P   T   I   100


361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q   P   T   Q   P   T   T   Q   L   P   T   D   S   P   T   Q   P   T   T   G   120


421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S   F   C   P   G   P   V   T   L   C   S   D   L   E   S   H   S   T   E   A   140


481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGGAATG 540
141 V   L   G   D   A   L   V   D   F   S   L   K   L   Y   H   A   F   S   G̲   M   160


541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K   K   V   E   T   N   M   A   F   S   P   F   S   I   A   S   L   L   T   Q   180


601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V   L   L   G   A   G   Q   N   T   K   T   N   L   E   S   I   L   S   Y   P   200


661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K   D   F   T   C   V   H   Q   A   L   K   G   F   T   T   K   G   V   T   S   220


721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V   S   Q   I   F   H   S   P   D   L   A   I   R   D   T   F   V   N   A   S   240


781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R   T   L   Y   S   S   S   P   R   V   L   S   N   N   S   D   A   N   L   E   260


841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L   I   N   T   W   V   A   K   N   T   N   N   K   I   S   R   L   L   D   S   280


901 CTGCCCTCCG ATACCCGCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L   P   S   D   T   R   L   V   L   L   N   A   I   Y   L   S   A   K   W   K   300
```

Figure 14B

```
 961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T  T  F  D     P  K  K     T  R  M     E  P  F     H  F  K  N     S  V  I  320


1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTTG 1080
 321 K  V  P  M     M  N  S     K  K  Y     P  V  A     H  F  I  D     Q  T  L  340


1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K  A  K  V     G  Q  L     Q  L  S     H  N  L  S     L  V  I     L  V  P  360


1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q  N  L  K     H  R  L     E  D  M     E  Q  A  L     S  P  S     V  F  K  380


1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A  I  M  E     K  L  E     M  S  K     F  Q  P  T     L  L  T     L  P  R  400


1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I  K  V  T     T  S  Q     D  M  L     S  I  M  E     K  L  E     F  F  D  420


1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
 421 F  S  Y  D     L  N  L     C  G  L     T  E  D  P     D  L  Q     V  S  A  440


1381 ATGCAGCACC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M  Q  H  Q     T  V  L     E  L  T     E  T  G  V     E  A  A     A  A  S  460


1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A  I  S  V     A  R  T     L  L  V     F  E  V  Q     Q  P  F     L  F  V  480


1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L  W  D  Q     Q  H  K     F  P  V     F  M  G  R     V  Y  D     P  R  A  500


1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620


1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680


1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740


1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800


1801 TCTATAAATA AAACCTGACA GACCAT 1826
```

Figure 15A

```
  1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCCAG 60


 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
  1 M  A  S    R  L  T  L   L  T  L    L  L  L  L   L  A  G    D  R  A   20


121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S  S  N  P  N  A  T   S  S  S    S  Q  D  P   E  S  L    Q  D  R   40


181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G  E  G    K  V  A  T   T  V  I    S  K  M  L   F  V  E    P  I  L   60


241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E  V  S    S  L  P  T   T  N  S    T  T  N  S   A  T  K    I  T  A   80


301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N  T  T  D  E  P  T   T  Q  P    T  T  E  P   T  T  Q    P  T  I   100


361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q  P  T  Q  P  T  T   Q  L  P    T  D  S  P   T  Q  P    T  T  G   120


421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S  F  C  P  G  P  V   T  L  C    S  D  L  E   S  H  S    T  E  A   140


481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V  L  G  D  A  L  V   D  F  S    L  K  L  Y   H  A  F    S  A  M   160


541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K  K  V  E  T  N  M   A  F  S    P  F  S  I   A  S  L    L  T  Q   180


601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V  L  L  G  A  G  Q   N  T  K    T  N  L  E   S  I  L    S  Y  P   200


661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K  D  F  T  C  V  H   Q  A  L    K  G  F  T   K  G  V    T  S   220


721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V  S  Q  I  F  H  S   P  D  L    A  I  R  D   T  F  V    N  A  S   240


781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R  T  L  Y  S  S  S   P  R  V    L  S  N  N   S  D  A    N  L  E   260


841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L  I  N  T  W  V  A   K  N  T    N  N  K  I   S  R  L    L  D  S   280


901 CTGCCCTCCG ATACCCGCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L  P  S  D  T  R  L   V  L  L    N  A  I  Y   L  S  A    K  W  K   300
```

Figure 15B

```
 961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T   T   F   D   P   K   K   T   R   M   E   P   F   H   F   K   N   S   V   I   320


1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTTG 1080
·321 K   V   P   M   M   N   S   K   K   Y   P   V   A   H   F   I   D   Q   T   L   340


1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K   A   K   V   G   Q   L   Q   L   S   H   N   L   S   L   V   I   L   V   P   360


1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q   N   L   K   H   R   L   E   D   M   E   Q   A   L   S   P   S   V   F   K   380


1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A   I   M   E   K   L   E   M   S   K   F   Q   P   T   L   L   T   L   P   R   400


1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I   K   V   T   T   S   Q   D   M   L   S   I   M   E   K   L   E   F   F   D   420


1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
 421 F   S   Y   D   L   N   L   C   G   L   T   E   D   P   D   L   Q   V   S   A   440


1381 ATGCAGCACC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M   Q   H   Q   T   V   L   E   L   T   E   T   G   V   E   A   A   A   S   460


1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCATG 1500
 461 A   I   S   V   A   R   T   L   L   V   F   E   V   Q   Q   P   F   L   F   M   480


1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L   W   D   Q   Q   H   K   F   P   V   F   M   G   R   V   Y   D   P   R   A   500


1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620


1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680


1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740


1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800


1801 TCTATAAATA AAACCTGACA GACCAT 1826
```

Figure 16

```
  1 TCCTCCACCT GCTGGCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
  1                                         M   W   F   L   V   L   C   L    8


 61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
  9 A   L   S   L   G   G   T   G   A   A   P   P   I   Q   S   R   I   V   G   G   28


121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATTT CAGCACTTTC 180
 29 W   E   C   E   Q   H   S   Q   P   W   Q   A   A   L   Y   H   F   S   T   F   48


181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q   C   G   G   I   L   V   H   R   Q   W   V   L   T   A   A   H   C   I   S   68


241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAAA CACAGCCCAG 300
 69 D   N   Y   Q   L   W   L   G   R   H   N   L   F   D   D   E   N   T   A   Q   88


301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F   V   H   V   S   E   S   F   P   H   P   G   F   N   M   S   L   L   E   N   108


361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
109 H   T   R   Q   A   D   E   D   Y   S   H   D   L   M   L   L   R   L   T   E   128


421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCACCGA GGAACCCGAA 480
129 P   A   D   T   I   T   D   A   V   K   V   V   E   L   P   T   E   E   P   E   148


481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
149 V   G   S   T   C   L   A   S   G   W   G   S   I   E   P   E   N   F   S   F   168


541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CAAAAAAGCC 600
169 P   D   D   L   Q   C   V   D   L   K   I   L   P   N   D   E   C   K   K   A   188


601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
189 H   V   Q   K   V   T   D   F   M   L   C   V   G   H   L   E   G   G   K   D   208


661 ACCTGTGTGG GTGATTCAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
209 T   C   V   G   D   S   G   G   P   L   M   C   D   G   V   L   Q   G   V   T   228


721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
229 S   W   G   Y   V   P   C   G   T   P   N   K   P   S   V   A   V   R   V   L   248


781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
249 S   Y   V   K   W   I   E   D   T   I   A   E   N   S   *                     262


841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871
```

Figure 17

```
  1 TCCTCCACCT GCTGGCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC  60
  1                                           M  W  F  L  V  L  C  L   8

 61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
  9 A  L  S  L  G  G  T  G  A  A  P  P  I  Q  S  R  I  V  G  G   28

121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATTT CAGCACTTTC 180
 29 W  E  C  E  Q  H  S  Q  P  W  Q  A  A  L  Y  H  F  S  T  F   48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q  C  G  G  I  L  V  H  R  Q  W  V  L  T  A  A  H  C  I  S   68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAAA CACAGCCCAG 300
 69 D  N  Y  Q  L  W  L  G  R  H  N  L  F  D  D  E  N  T  A  Q   88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F  V  H  V  S  E  S  F  P  H  P  G  F  N  M  S  L  L  E  N  108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
109 H  T  R  Q  A  D  E  D  Y  S  H  D  L  M  L  L  R  L  T  E  128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCACCGA GGAACCCGAA 480
129 P  A  D  T  I  T  D  A  V  K  V  V  E  L  P  T  E  E  P  E  148

481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
149 V  G  S  T  C  L  A  S  G  W  G  S  I  E  P  E  N  F  S  F  168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CGAAAAAGCC 600
169 P  D  D  L  Q  C  V  D  L  K  I  L  P  N  D  E  C  E  K  A  188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
189 H  V  Q  K  V  T  D  F  M  L  C  V  G  H  L  E  G  G  K  D  208

661 ACCTGTGTGG GTGATTCAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
209 T  C  V  G  D  S  G  G  P  L  M  C  D  G  V  L  Q  G  V  T  228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
229 S  W  G  Y  V  P  C  G  T  P  N  K  P  S  V  A  V  R  V  L  248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
249 S  Y  V  K  W  I  E  D  T  I  A  E  N  S  *           262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871
```

Figure 18

```
  1 TCCTCCACCT GCTGGCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC  60
  1                                            M  W  F  L  V  L  C  L   8

 61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
  9 A  L  S  L  G  G  T  G  A  A  P  P  I  Q  S  R  I  V  G  G  28

121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATTT CAGCACTTTC 180
 29 W  E  C  E  Q  H  S  Q  P  W  Q  A  A  L  Y  H  F  S  T  F  48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q  C  G  G  I  L  V  H  R  Q  W  V  L  T  A  A  H  C  I  S  68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAAA CACAGCCCAG 300
 69 D  N  Y  Q  L  W  L  G  R  H  N  L  F  D  D  E  N  T  A  Q  88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F  V  H  V  S  E  S  F  P  H  P  G  F  N  M  S  L  L  E  N  108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
109 H  T  R  Q  A  D  E  D  Y  S  H  D  L  M  L  L  R  L  T  E  128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCACCCA GGAACCCGAA 480
129 P  A  D  T  I  T  D  A  V  K  V  V  E  L  P  T  Q  E  P  E  148

481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
149 V  G  S  T  C  L  A  S  G  W  G  S  I  E  P  E  N  F  S  F  168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CAAAAAAGCC 600
169 P  D  D  L  Q  C  V  D  L  K  I  L  P  N  D  E  C  K  K  A  188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
189 H  V  Q  K  V  T  D  F  M  L  C  V  G  H  L  E  G  G  K  D  208

661 ACCTGTGTGG GTGATTCAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
209 T  C  V  G  D  S  G  G  P  L  M  C  D  G  V  L  Q  G  V  T  228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
229 S  W  G  Y  V  P  C  G  T  P  N  K  P  S  V  A  V  R  V  L  248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
249 S  Y  V  K  W  I  E  D  T  I  A  E  N  S  *                   262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871
```

Figure 19

```
BRB1_MOUSE  MASQ.ASLKLQPSNQSQQAPPNITSCEGAPEAWDLLCRVLPGFVITVCFFGLLGNLLVLS
BRB1_RAT    MASE.VLLELQPSNRSLQAPANITSCESALEDWDLLYRVLPGFVITICFFGLLGNLLVLS
BRB1_HUMAN  MASSWPPLELQSSNQSQLFPQNATACDNAPEAWDLLHRVLPTFIISICFFGLLGNLFVLL
BRB1_RABIT  MASQ.GPLELQPSNQSQLAPPNATSCSGAPDAWDLLHRLLPTFIIAIFTLGLLGNSFVLS

BRB1_MOUSE  FFLLPWRRWW...QQRRQRLTIAEIYLANLAASDLVFVLGLPFWAENVGNRFNWPFGSDL
BRB1_RAT    FFLLPWRQWWWQQRQRQQRLTIAEIYLANLAASDLVFVLGLPFWAENIGNRFNWPFGTDL
BRB1_HUMAN  VFLLP..........RRQLNVAEIYLANLAASDLVFVLGLPFWAENIWNQFNWPFGALL
BRB1_RABIT  VFLLA..........RRRLSVAEIYLANLAASDLVFVLGLPFWAENVRNQFDWPFGAAL

BRB1_MOUSE  CRVVSGVIKANLFISIFLVVAISQDRYRLLVYPMTSWGNRRRRQAQVTCLLIWVAGGLLS
BRB1_RAT    CRVVSGVIKANLFVSIFLVVAISQDRYRLLVYPMTSWGYRRRRQAQATCLLIWVAGGLLS
BRB1_HUMAN  CRVINGVIKANLFISIFLVVAISQDRYRVLVHPMASGROQRRRQARVTCVLIWVVGGLLS
BRB1_RABIT  CRIVNGVIKANLFISIFLVVAISQDRYSVLVHPMASRRGRRRRQAQATCALIWLAGGLLS

BRB1_MOUSE  TPTFLLRSVKVVPDLNISACILLFPHEAWHFVRMVELNVLGFLLPLAAILYFNFHILASL
BRB1_RAT    IPTFLLRSVKVVPDLNVSACILLFPHEAWHFARMVELNVLGFLLPVTAIVFFNYHILASL
BRB1_HUMAN  IPTFLLRSLQAVPDLNITACILLLPHEAWHFARIIVELNILGFLLPLAAIVFFNYHILASL
BRB1_RABIT  TPTFVLRSVRAVPELNVSACILLLPHEAWHWLRMVELNLLGFLLPLAAILFFNCHILASL

                                         *
BRB1_MOUSE  RGQKEASRTRCGGPKDSKTMCLILTLVASFLVCWAPYHFFAFLDFLVQVRVIQDCFWKEL
BRB1_RAT    RGQKEASRTRCGGPKGSKTTCLILTLVASFLVCWCPYHFFAFLDFLVQVRVIQDCSWKEI
BRB1_HUMAN  RTREEVSRTRVRGPKDSKTTALILTLVVAFLVCWAPYHFFAFLEFLFQVQAVRGCFWEDF
BRB1_RABIT  RRRGERVPSRCGGPRDSKSTALILTLVASFLVCWAPYHFFAFLECLWQVHAIGGCFWEEF

                              *
BRB1_MOUSE  TDLGLQLANFFAFVNSCLNPLIYVFAG  LFKTRVLGTL~~~~~~~~~~~~~~~~~~~~~
BRB1_RAT    TDLGLQLANFFAFVNSCLNPLIYVFAG  LLKTRVLGTL~~~~~~~~~~~~~~~~~~~~~
BRB1_HUMAN  IDLGLQLANFFAFTNSSLNPVIYVFVG  LFRTKVWELYKQCTPKSLAPISSSHRKEIFQL
BRB1_RABIT  TDLGLQLSNFSAFVNSCLNPVIYVFVG  LFRTKVWELCQQCSPRSLAPVSSSRRKEMLWG

BRB1_MOUSE  ~~~~
BRB1_RAT    ~~~~
BRB1_HUMAN  FWRN
BRB1_RABIT  FWRN
```

Figure 20

```
BRB2_MOUSE  ~~~~~MPCSWKLLGFLSVHE.PMPTAASFGIEMFNVTTQVLGSALNGTLSKDN.CPDTEW
BRB2_RAT    MDTRSSLCP.KTQAVVAVFW.GPGCHLSTCIEMFNITTQALGSAHNGTFSEVN.CPDTEW
BRB2_RABIT  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~MLNITSQVLAPALNGSVSQSSGCPNTEW
BRB2_CAVPO  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~MFNITSQV..SALNATLAQGNSCLDAEW
BRB2_HUMAN  ~~~~~MFSPWKISMFLSVREDSVPTTASFSADMLNVTLQ...GPTLNGTFAQ.SKCPQVEW

BRB2_MOUSE  WSWLNAIQAPFLWVLFLLAALENIFVLSVFFLHKNSCTVAEIYLGNLAAADLILACGLPF
BRB2_RAT    WSWLNAIQAPFLWVLFLLAALENIFVLSVFCLHKTNCTVAEIYLGNLAAADLILACGLPF
BRB2_RABIT  SGWLNVIQAPFLWVLFVLATLENIFVLSVFCLHKSSCTVAEMYLGNLAAADLILACGLPF
BRB2_CAVPO  WSWLNTIQAPFLWVLFVLAVLENIFVLSVFFLHKSSCTVAEIYLGNLAVADLILAFGLPF
BRB2_HUMAN  LGWLNTIQPPFLWVLFVLATLENIFVLSVFCLHKSSCTVAEIYLGNLAAADLILACGLPF

BRB2_MOUSE  WAITIANNFDWVFGEVLCRVVNTMIYMNLYSSICFLMLVSIDRYLALVKTMSMGRMRGVR
BRB2_RAT    WAITIANNFDWLFGEVLCRVVNTMIYMNLYSSICFLMLVSIDRYLALVKTMSMGRMRGVR
BRB2_RABIT  WAVTIANHFDWLFGEALCRVVNTMIYMNLYSSICFLMLVSIDRYLALVKTMSIGRMRRVR
BRB2_CAVPO  WAITIANNFDWLFGEVLCRMVNTMIQMNMYSSICFLMLVSIDRYLALVKTMSMGRMRGVR
BRB2_HUMAN  WAITISNNFDWLFGETLCRVVNATISMNLYSSICFLMLVSIDRYLALVKTMSMGRMRGVR

BRB2_MOUSE  WAKLYSLVIWGCTLLLSSPMLVFRTMREYSEEGHNVTACVIYPSRSWEVFTNVLLNLVG
BRB2_RAT    WAKLYSLVIWSCTLLLSSPMLVFRTMKDYREEGHNVTACVIYPSRSWEVFTNMLLNLVG
BRB2_RABIT  WAKLYSLVIWGCTLLLSSPMLVFRTMKDYRDEGYNVTACIIDYPSRSWEVFTNVLLNLVG
BRB2_CAVPO  WAKLYSLVIWGCALLLSSPMLVFRTMKDYRDEGHNVTACLIIYPSLIWQVFTNVLLNLVG
BRB2_HUMAN  WAKLYSLVIWGCTLLLSSPMLVFRTMKEYSDEGHNVTACVISYPSLIWEVFTNMLLNVVG

BRB2_MOUSE  FLLPLSVITFCTVRILQVLRNNEMKKFKEVQTERKATVLVLAVLGLFVLCWMPFQISTFL
BRB2_RAT    FLLPLSIITFCTVRIMQVLRNNEMKKFKEVQTEKKATVLVLAVLGLFVLCWFPFQISTFL
BRB2_RABIT  FLLPLSVITFCTVQILQVLRNNEMQKFKEIQTERRATVLVLAVLLLFVVCWLPFQVSTFL
BRB2_CAVPO  FLLPLSIITFCTVQIMQVLRNNEMQKFKEIQTERRATVLVLAVLLLFVVCWLPFQIGTFL
BRB2_HUMAN  FLLPLSVITFCTMQIMQVLRNNEMQKFKEIQTERRATVLVLVVLLLFIICWLPFQISTFL

BRB2_MOUSE  DTLLRLGVLSGCWDEHAVDVITQISSYVAYSNSGLNPLVYVIVGKRFRKKSREVYRVLCQ
BRB2_RAT    DTLLRLGVLSGCWNERAVDIVTQISSYVAYSNSCLNPLVYVIVGKRFRKKSREVYQAICR
BRB2_RABIT  DTLLKLGVLSSCWDEHVIDVITQVGSFMGYSNSCLNPLVYVIVGKRFRKKSREVYRAACP
BRB2_CAVPO  DTLRLLGFLPGCW.EHVIDLITQISSYLAYSNSCLNPLVYVIVGKRFRKKSREVYHGICR
BRB2_HUMAN  DTLHRLGTLSSCQDERIIDVITQIASFMAYSNSCLNPLVYVIVGKRFRKKSWEVYQGVCQ

                *

BRB2_MOUSE  K GCMGEPVQMENSMGTLRTSISVERQIHKLQDWAGKKQ~~~~~~~~
BRB2_RAT    K GCMGESVQMENSMGTLRTSISVDRQIHKLQDWAGNKQ~~~~~~~~
BRB2_RABIT  KAGCVLEPVQAESSMGTLRTSISVERQIHKLPEWTRSSQ~~~~~~~~
BRB2_CAVPO  S GCVSEPAQSENSMGTLRTSISVDRQIHKLQDWARSSSEGTPPGLL
BRB2_HUMAN  K GCRSEPIQMENSMGTLRTSISVERQIHKLQDWAGSRQ~~~~~~~~
```

Figure 21A

```
  1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC  60
  1      M    S    S    W    P    P    L    E    Q    S    S    N    Q    S    Q    L   18


 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19  F    P    Q    N    A    T    A    C    D    N    A    P    E    A    W    D    L    L    H    R   38


121 GTGCTGCCNA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39  V    L    P    T    F    I    I    S    I    C    F    F    G    L    L    G    N    L    F    V   58


181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59  L    L    V    F    L    L    P    R    R    Q    L    N    V    A    E    I    Y    L    A    N   78


241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79  L    A    A    S    D    L    V    F    V    L    G    L    P    F    W    A    E    N    I    W   98


301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAANGG GGTCATCAAG 360
 99  N    Q    F    N    W    P    F    G    A    L    L    C    R    V    I    N    G    V    I    K  118


361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119  A    N    L    F    I    S    I    F    L    V    V    A    I    S    Q    D    R    Y    R    V  138


421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GNCAGGCCCG GGTCACCTGC 480
139  L    V    H    P    M    A    S    G    R    Q    Q    R    R    R    Q    A    R    V    T    C  158


481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159  V    L    I    W    V    V    G    G    L    L    S    I    P    T    F    L    L    R    S    I  178


541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCNTGC TCCTCCCCCA TGAGGCCTGG 600
179  Q    A    V    P    D    L    N    I    T    A    C    I    X    L    L    P    H    E    A    W  198


601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199  H    F    A    R    I    V    E    L    N    I    L    G    F    L    L    P    L    A    A    I  218


661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGANGAGGT CAGCAGGACA 720
219  V    F    F    N    Y    H    I    L    A    S    L    R    T    R    E    E    V    S    R    T  238


721 AGAGTGCNGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239  R    V    X    G    P    K    D    S    K    T    T    A    L    I    L    T    L    V    V    A  258


781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259  F    L    V    C    W    A    P    Y    H    F    F    A    F    L    E    F    L    F    Q    V  278


841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279  Q    A    V    R    G    C    F    W    E    D    F    I    D    L    G    L    Q    L    A    N  298
```

Figure 21B

```
901  TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCNGCTC 960
299  F  F  A  F   T  N  S    S  L  N    P  V  I  Y    V  F  V    G  X  L   318


961  TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319  F  R  T  K   V  W  E    L  Y  K    Q  C  T  P    K  S  L    A  P  I   338


1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339  S  S  S  H   R  K  E    I  F  Q    L  F  W  R    N  *                353
```

1081 CC 1082

Figure 22A

```
  1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60

 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120

121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180

181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
  1                                     M   D   N   V   L   P   V   D   S   D   10

241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L   S   P   N   I   S   T   N   T   S   E   P   N   Q   F   V   Q   P   A   W   30

301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q   I   V   L   W   A   A   A   Y   T   V   I   V   V   T   S   V   V   G   N   50

361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V   V   V   M   W   I   I   L   A   H   K   R   M   R   T   V   T   N   Y   F   70

421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L   V   N   L   A   F   A   E   A   S   M   A   A   F   N   T   V   V   N   F   90

481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACTTC 540
 91 T   Y   A   V   H   N   E   W   Y   Y   G   L   F   Y   C   K   F   H   N   F   110

541 TTNCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
111 F   P   I   A   V   F   A   S   I   Y   S   M   T   A   V   A   F   D   R   130

601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
131 Y   M   A   I   I   H   P   L   Q   P   R   L   S   A   T   A   T   K   V   V   150

661 ATCTGTGTCA TNTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
151 I   C   V   I   W   V   L   A   L   L   L   A   F   P   Q   G   Y   Y   S   T   170

721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
171 T   E   T   M   P   S   R   V   V   C   M   I   E   W   P   E   H   P   N   K   190

781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
191 I   Y   E   K   V   Y   H   I   C   V   T   V   L   I   Y   F   L   P   L   L   210

841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
211 V   I   G   Y   A   Y   T   V   V   G   I   T   L   W   A   S   E   I   P   G   230

901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
231 D   S   S   D   R   Y   H   E   Q   V   S   A   K   R   K   V   V   K   M   M   250
```

D0053 NP

Figure 22B

```
 961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCTCCTG 1020
 251 I  V  V    C  T  F    A  I  C    W  L  P    F  H  I  F    F  L  L  270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P  Y  I  N  P  D  L    Y  L  K    K  F  I  Q    Q  V  Y    L  A  I  290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M  W  L  A  M  S  S    T  M  Y    N  P  I  I    Y  C  C    L  N  D  310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R  F  R  L  G  F  K    H  A  F    R  C  C  P    F  I  S    A  G  D  330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y  E  G  L  E  M  K    S  T  R    Y  L  Q  T    Q  G  S    V  Y  K  350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V  S  R  L  E  T  T    I  S  T    V  V  G  A    H  E  E    E  P  E  370

1321 GACGGCCCCA AGGCCACACC CTCNTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D  G  P  K  A  T  P    S  S  L    D  L  T  S    N  C  S    S  R  S  390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D  S  K  T  M  T  E    S  F  S    F  S  S  N    V  L  S    *       407

1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766
```

Figure 23A

```
  1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCCAG 60


 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
  1 M   A   S   R   L   T   L   L   T   L   L   L   L   L   A   G   D   R   A   20


121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S   S   N   P   N   A   T   S   S   S   Q   D   P   E   S   L   Q   D   R   40


181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGNTGA ACCCATCCTG 240
 41 G   E   G   K   V   A   T   T   V   I   S   K   M   L   F   X   E   P   I   L   60


241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E   V   S   L   P   T   T   N   S   T   T   N   S   A   T   K   I   T   A   80


301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N   T   T   D   E   P   T   T   Q   P   T   T   E   P   T   T   Q   P   T   I   100


361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q   P   T   Q   P   T   T   Q   L   P   T   D   S   P   T   Q   P   T   T   G   120


421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S   F   C   P   G   P   V   T   L   C   S   D   L   E   S   H   S   T   E   A   140


481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGNAATG 540
141 V   L   G   D   A   L   V   D   F   S   L   K   L   Y   H   A   F   S   X   M   160


541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K   K   V   E   T   N   M   A   F   S   P   F   S   I   A   S   L   L   T   Q   180


601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V   L   L   G   A   G   Q   N   T   K   T   N   L   E   S   I   L   S   Y   P   200


661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K   D   F   T   C   V   H   Q   A   L   K   G   F   T   K   G   V   T   S   220


721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V   S   Q   I   F   H   S   P   D   L   A   I   R   D   T   F   V   N   A   S   240


781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R   T   L   Y   S   S   S   P   R   V   L   S   N   N   S   D   A   N   L   E   260


841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L   I   N   T   W   V   A   K   N   T   N   N   K   I   S   R   L   L   D   S   280


901 CTGCCCTCCG ATACCCGCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L   P   S   D   T   R   L   V   L   L   N   A   I   Y   L   S   A   K   W   K   300
```

Figure 23B

```
 961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T   T  F  D   P  K  K   T  R  M   E  P  F  H   F  K  N   S  V  I  320


1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTTG 1080
 321 K  V  P  M   M  N  S   K  K  Y   P  V  A  H   F  I  D   Q  T  L  340


1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K  A  K  V   G  Q  L   Q  L  S   H  N  L  S   L  V  I   L  V  P  360


1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q  N  L  K   H  R  L   E  D  M   E  Q  A  L   S  P  S   V  F  K  380


1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A  I  M  E   K  L  E   M  S  K   F  Q  P  T   L  L  T   L  P  R  400


1261 ATCAAAGTGA CGACCAGNCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I  K  V  T   T  S  Q   D  M  L   S  I  M  E   K  L  E   F  F  D  420


1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
 421 F  S  Y  D   L  N  L   C  G  L   T  E  D  P   D  L  Q   V  S  A  440


1381 ATGCAGCACC AGACAGTGCT GGAACTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M  Q  H  Q   T  V  L   E  L  T   E  T  G  V   E  A  A   A  A  S  460


1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCNTG 1500
 461 A  I  S  V   A  R  T   L  L  V   F  E  V  Q   Q  P  F   L  F  X  480


1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L  W  D  Q   Q  H  K   F  P  V   F  M  G  R   V  Y  D   P  R  A  500


1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620


1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680


1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740


1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800


1801 TCTATAAATA AAACCTGACA GACCAT 1826
```

Figure 24

```
  1 TCCTCCACCT GCTGGCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC  60
  1                                         M   W   F   L   V   L   C   L    8

 61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
  9 A   L   S   L   G   G   T   G   A   A   P   P   I   Q   S   R   I   V   G   G   28

121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATTT CAGCACTTTC 180
 29 W   E   C   E   Q   H   S   Q   P   W   Q   A   A   L   Y   H   F   S   T   F   48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q   C   G   G   I   L   V   H   R   Q   W   V   L   T   A   A   H   C   I   S   68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAAA CACAGCCCAG 300
 69 D   N   Y   Q   L   W   L   G   R   H   N   L   F   D   D   E   N   T   A   Q   88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F   V   H   V   S   E   S   F   P   H   P   G   F   N   M   S   L   L   E   N  108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
109 H   T   R   Q   A   D   E   D   Y   S   H   D   L   M   L   L   R   L   T   E  128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCACCNA GGAACCCGAA 480
129 P   A   D   T   I   T   D   A   V   K   V   V   E   L   P   T   X   E   P   E  148

481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
149 V   G   S   T   C   L   A   S   G   W   G   S   I   E   P   E   N   F   S   F  168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CNAAAAAGCC 600
169 P   D   D   L   Q   C   V   D   L   K   I   L   P   N   D   E   C   X   K   A  188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
189 H   V   Q   K   V   T   D   F   M   L   C   V   G   H   L   E   G   G   K   D  208

661 ACCTGTGTGG GTGATTCAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
209 T   C   V   G   D   S   G   G   P   L   M   C   D   G   V   L   Q   G   V   T  228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
229 S   W   G   Y   V   P   C   G   T   P   N   K   P   S   V   A   V   R   V   L  248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
249 S   Y   V   K   W   I   E   D   T   I   A   E   N   S   *                    262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871
```

Figure 25A

```
  1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC  60
  1     M    A    S    S    W    P    P    L    E    L    Q    S    S    N    Q    S    Q    L   18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19   F    P    Q    N    A    T    A    C    D    N    A    P    E    A    W    D    L    L    H    R   38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39   V    L    P    T    F    I    I    S    I    C    F    F    G    L    L    G    N    L    F    V   58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59   L    L    V    F    L    L    P    R    R    Q    L    N    V    A    E    I    Y    L    A    N   78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT CTGGGCAGA GAATATCTGG 300
 79   L    A    A    S    D    L    V    F    V    L    G    L    P    F    W    A    E    N    I    W   98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAATGG GGTCATCAAG 360
 99   N    Q    F    N    W    P    F    G    A    L    L    C    R    V    I    N    G    V    I    K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119   A    N    L    F    I    S    I    F    L    V    V    A    I    S    Q    D    R    Y    R    V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139   L    V    H    P    M    A    S    G    R    Q    Q    R    R    R    Q    A    R    V    T    C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159   V    L    I    W    V    V    G    G    L    L    S    I    P    T    F    L    L    R    S    I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179   Q    A    V    P    D    L    N    I    T    A    C    I    L    L    L    P    H    E    A    W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199   H    F    A    R    I    V    E    L    N    I    L    G    F    L    L    P    L    A    A    I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219   V    F    F    N    Y    H    I    L    A    S    L    R    T    R    E    E    V    S    R    T  238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239   R    V    R    G    P    K    D    S    K    T    T    A    L    I    L    T    L    V    V    A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259   F    L    V    C    W    A    P    Y    H    F    F    A    F    L    E    F    L    F    Q    V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279   Q    A    V    R    G    C    F    W    E    D    F    I    D    L    G    L    Q    L    A    N  298
```

Figure 25B

```
 901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC  960
 299 F    F    A    F      T    N    S      S    L    N      P    V    I    Y      V    F    V      G    R    L    318


 961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
 319 F    R    T    K      V    W    E      L    Y    K      Q    C    T    P      K    S    L      A    P    I    338


1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S    S    S    H      R    K    E      I    F    Q      L    F    W    R      N    *                338
                                                                                                            353

1081 CC 1082
```

Figure 26A

```
  1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
  1     M    S    S    W    P    P    L    E    L    Q    S    S    N    Q    S    Q    L   18


 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F    P    Q    N    A    T    A    C    D    N    A    P    E    A    W    D    L    L    H    R   38


121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39 V    L    P    T    F    I    I    S    I    C    F    F    G    L    L    G    N    L    F    V   58


181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L    L    V    F    L    L    P    R    R    Q    L    N    V    A    E    I    Y    L    A    N   78


241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L    A    A    S    D    L    V    F    V    L    G    L    P    F    W    A    E    N    I    W   98


301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N    Q    F    N    W    P    F    G    A    L    L    C    R    V    I    N    G    V    I    K  118


361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A    N    L    F    I    S    I    F    L    V    V    A    I    S    Q    D    R    Y    R    V  138


421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GACAGGCCCG GGTCACCTGC 480
139 L    V    H    P    M    A    S    G    R    Q    Q    R    R    R    Q    A    R    V    T    C  158


481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V    L    I    W    V    V    G    G    L    L    S    I    P    T    F    L    L    R    S    I  178


541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q    A    V    P    D    L    N    I    T    A    C    I    L    L    L    P    H    E    A    W  198


601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H    F    A    R    I    V    E    L    N    I    L    G    F    L    L    P    L    A    A    I  218


661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V    F    F    N    Y    H    I    L    A    S    L    R    T    R    E    E    V    S    R    T  238


721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R    V    R    G    P    K    D    S    K    T    T    A    L    I    L    T    L    V    V    A  258


781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F    L    V    C    W    A    P    Y    H    F    F    A    F    L    E    F    L    F    Q    V  278


841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q    A    V    R    G    C    F    W    E    D    F    I    D    L    G    L    Q    L    A    N  298
```

Figure 26B

```
 901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC  960
 299 F    F    A    F    T    N    S    S    L    N    P    V    I    Y    V    F    V    G    R    L    318


 961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
 319 F    R    T    K    V    W    E    L    Y    K    Q    C    T    P    K    S    L    A    P    I    338


1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S    S    S    H    R    K    E    I    F    Q    L    F    W    R    N    *              353


1081 CC 1082
```

Figure 27A

```
  1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC  60
  1     M    A    S    S    W    P    P    L    E    L    Q    S    S    N    Q    S    Q    L   18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F    P    Q    N    A    T    A    C    D    N    A    P    E    A    W    D    L    L    H    R   38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39 V    L    P    T    F    I    I    S    I    C    F    F    G    L    L    G    N    L    F    V   58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L    L    V    F    L    L    P    R    R    Q    L    N    V    A    E    I    Y    L    A    N   78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L    A    A    S    D    L    V    F    V    L    G    L    P    F    W    A    E    N    I    W   98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N    Q    F    N    W    P    F    G    A    L    L    C    R    V    I    N    G    V    I    K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A    N    L    F    I    S    I    F    L    V    V    A    I    S    Q    D    R    Y    R    V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139 L    V    H    P    M    A    S    G    R    Q    Q    R    R    R    Q    A    R    V    T    C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V    L    I    W    V    V    G    G    L    L    S    I    P    T    F    L    L    R    S    I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCGTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q    A    V    P    D    L    N    I    T    A    C    I    V    L    L    P    H    E    A    W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H    F    A    R    I    V    E    L    N    I    L    G    F    L    L    P    L    A    A    I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V    F    F    N    Y    H    I    L    A    S    L    R    T    R    E    E    V    S    R    T  238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R    V    R    G    P    K    D    S    K    T    T    A    L    I    L    T    L    V    V    A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F    L    V    C    W    A    P    Y    H    F    F    A    F    L    E    F    L    F    Q    V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q    A    V    R    G    C    F    W    E    D    F    I    D    L    G    L    Q    L    A    N  298
```

Figure 27B

```
 901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC  960
 299 F    F    A    F    T    N    S    S    L    N    P    V    I    Y    V    F    V    G    R    L     318


 961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
 319 F    R    T    K    V    W    E    L    Y    K    Q    C    T    P    K    S    L    A    P    I     338


1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S    S    S    H    R    K    E    I    F    Q    L    F    W    R    N    *                        353


1081 CC 1082
```

Figure 28A

```
  1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC  60
  1        M   A   S   S   W   P   P   L   E   L   Q   S   S   N   Q   S   Q   L   18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19    F   P   Q   N   A   T   A   C   D   N   A   P   E   A   W   D   L   L   H   R   38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39    V   L   P   T   F   I   I   S   I   C   F   F   G   L   L   G   N   L   F   V   58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59    L   L   V   F   L   L   P   R   R   Q   L   N   V   A   E   I   Y   L   A   N   78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79    L   A   A   S   D   L   V   F   V   L   G   L   P   F   W   A   E   N   I   W   98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99    N   Q   F   N   W   P   F   G   A   L   L   C   R   V   I   N   G   V   I   K  118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119    A   N   L   F   I   S   I   F   L   V   V   A   I   S   Q   D   R   Y   R   V  138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139    L   V   H   P   M   A   S   G   R   Q   Q   R   R   R   Q   A   R   V   T   C  158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159    V   L   I   W   V   V   G   G   L   L   S   I   P   T   F   L   L   R   S   I  178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179    Q   A   V   P   D   L   N   I   T   A   C   I   L   L   L   P   H   E   A   W  198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199    H   F   A   R   I   V   E   L   N   I   L   G   F   L   L   P   L   A   A   I  218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA·720
219    V   F   F   N   Y   H   I   L   A   S   L   R   T   R   K̲   E   V   S   R   T  238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239    R   V   R   G   P   K   D   S   K   T   T   A   L   I   L   T   L   V   V   A  258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259    F   L   V   C   W   A   P   Y   H   F   F   A   F   L   E   F   L   F   Q   V  278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279    Q   A   V   R   G   C   F   W   E   D   F   I   D   L   G   L   Q   L   A   N  298
```

Figure 28B

```
 901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC  960
 299 F   F   A   F    T   N   S    S   L   N    P   V   I   Y    V   F   V    G   R   L   318


 961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
 319 F   R   T   K    V   W   E    L   Y   K    Q   C   T   P    K   S   L    A   P   I   338


1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S   S   S   H    R   K   E    I   F   Q    L   F   W   R    N   *                    353


1081 CC 1082
```

D0053 NP

Figure 29A

```
1   ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCACC  60
1   M  F  S  P  W  K  I  S  M  F  L  S  V  C  E  D  S  V  P  T   20

61  ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
21  T  A  S  F  S  A  D  M  L  N  V  T  L  Q  G  P  T  L  N  G   40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG CTGGCTCAA CACCATCCAG 180
41  T  F  A  Q  S  K  C  P  Q  V  E  W  L  G  W  L  N  T  I  Q   60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
61  P  P  F  L  W  V  L  F  V  L  A  T  L  E  N  I  F  V  L  S   80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81  V  F  C  L  H  K  S  S  C  T  V  A  E  I  Y  L  G  N  L  A  100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A  A  D  L  I  L  A  C  G  L  P  F  W  A  I  T  I  S  N  N  120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F  D  W  L  F  G  E  T  L  C  R  V  V  N  A  I  I  S  M  N  140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L  Y  S  S  I  C  F  L  M  L  V  S  I  D  R  Y  L  A  L  V  160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K  T  M  S  M  G  R  M  R  G  V  R  W  A  K  L  Y  S  L  V  180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
181 I  W  G  C  T  L  L  L  S  S  P  M  L  V  F  R  T  M  K  E  200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y  S  D  E  G  H  N  V  T  A  C  V  I  S  Y  P  S  L  I  W  220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E  V  F  T  N  M  L  L  N  V  V  G  F  L  L  P  L  S  V  I  240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T  F  C  T  M  Q  I  M  Q  V  L  R  N  N  E  M  Q  K  F  K  260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E  I  Q  T  E  R  R  A  T  V  L  V  L  V  V  L  L  F  I  280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I  C  W  L  P  F  Q  I  S  T  F  L  D  T  L  H  R  L  G  I  300
```

Figure 29B

```
 901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG  960
 301 L  S  S    Q  D  E    R  I  I    D  V  I  T   Q  I  A    S  F  M    320


 961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A  Y  S    N  S  C  L  N  P  L    V  Y  V  I   V  G  K    R  F  R    340


1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K  K  S    W  E  V  Y  Q  G  V    C  Q  K  G   G  C  R    S  E  P    360


1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I  Q  M    E  N  S  M   G  T  L    R  T  S  I   S  V  E    R  Q  I    380


1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H  K  L    Q  D  W  A   G  S  R    Q  *                              391


1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260


1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320


1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380


1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440


1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500


1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560


1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620


1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680


1681 GGTCCCTGAT AACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740


1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800


1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860


1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920


1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980


1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040
```

Figure 29C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100

2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160

2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220

2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280

2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340

2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400

2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460

2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520

2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580

2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640

2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700

2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760

2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820

2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880

2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940

2941 GAGGGCTAGA ACCTAGAAGG CTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000

3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060

3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120

3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180

3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTTAAA GCAAAGCGT GAAAAAAAG 3240

Figure 29D

```
3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAAAA AAA 3733
```

Figure 30A

```
  1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACC  60
  1 M  F  S  P  W  K  I  S  M  F  L  S  V  R  E  D  S  V  P  T  20


 61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
 21 T  A  S  F  S  A  D  M  L  N  V  T  L  Q  G  P  T  L  N  G  40


121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T  F  A  Q  S  K  C  P  Q  V  E  W  L  G  W  L  N  T  I  Q  60


181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
 61 P  P  F  L  W  V  L  F  V  L  A  T  L  E  N  I  F  V  L  S  80


241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V  F  C  L  H  K  S  S  C  T  V  A  E  I  Y  L  G  N  L  A 100


301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A  A  D  L  I  L  A  C  G  L  P  F  W  A  I  T  I  S  N  N 120


361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F  D  W  L  F  G  E  T  L  C  R  V  V  N  A  I  I  S  M  N 140


421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L  Y  S  S  I  C  F  L  M  L  V  S  I  D  R  Y  L  A  L  V 160


481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K  T  M  S  M  G  R  M  R  G  V  R  W  A  K  L  Y  S  L  V 180


541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
181 I  W  G  C  T  L  L  L  S  S  P  M  L  V  F  R  T  M  K  E 200


601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y  S  D  E  G  H  N  V  T  A  C  V  I  S  Y  P  S  L  I  W 220


661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E  V  F  T  N  M  L  L  N  V  V  G  F  L  L  P  L  S  V  I 240


721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T  F  C  T  M  Q  I  M  Q  V  L  R  N  N  E  M  Q  K  F  K 260


781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E  I  Q  T  E  R  R  A  T  V  L  V  L  V  V  L  L  F  I 280


841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I  C  W  L  P  F  Q  I  S  T  F  L  D  T  L  H  R  L  G  I 300
```

Figure 30B

```
 901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GACGTAATCA CACAGATCGC CTCCTTCATG  960
 301 L    S    S    C    Q    D    E    R    I    I    D    V    I    T    Q    I    A    S    F    M   320


 961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A    Y    S    N    S    C    L    N    P    L    V    Y    V    I    V    G    K    R    F    R   340


1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K    K    S    W    E    V    Y    Q    G    V    C    Q    K    G    G    C    R    S    E    P   360


1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I    Q    M    E    N    S    M    G    T    L    R    T    S    I    S    V    E    R    Q    I   380


1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H    K    L    Q    D    W    A    G    S    R    Q    *                                          391


1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260


1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320


1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380


1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440


1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500


1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560


1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620


1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680


1681 GGTCCCTGAT AACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740


1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800


1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860


1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920


1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980


1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040
```

Figure 30C

```
2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100

2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160

2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220

2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280

2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340

2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400

2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460

2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520

2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580

2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640

2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700

2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760

2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820

2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880

2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940

2941 GAGGGCTAGA ACCTAGAAGG CTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000

3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060

3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120

3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180

3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTTAAA GCAAAGCGT GAAAAAAAG 3240
```

Figure 30D

```
3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAAAA AAA 3733
```

Figure 31A

```
  1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACC  60
  1 M  F  S  P  W  K  I  S  M  F  L  S  V  R  E  D  S  V  P  T   20


 61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
 21 T  A  S  F  S  A  D  M  L  N  V  T  L  Q  G  P  T  L  N  G   40


121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T  F  A  Q  S  K  C  P  Q  V  E  W  L  G  W  L  N  T  I  Q   60


181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
 61 P  P  F  L  W  V  L  F  V  L  A  T  L  E  N  I  F  V  L  S   80


241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V  F  C  L  H  K  S  S  C  T  V  A  E  I  Y  L  G  N  L  A  100


301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A  A  D  L  I  L  A  C  G  L  P  F  W  A  I  T  I  S  N  N  120


361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F  D  W  L  F  G  E  T  L  C  R  V  V  N  A  I  I  S  M  N  140


421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L  Y  S  S  I  C  F  L  M  L  V  S  I  D  R  Y  L  A  L  V  160


481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K  T  M  S  M  G  R  M  R  G  V  R  W  A  K  L  Y  S  L  V  180


541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
181 I  W  G  C  T  L  L  L  S  S  P  M  L  V  F  R  T  M  K  E  200


601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y  S  D  E  G  H  N  V  T  A  C  V  I  S  Y  P  S  L  I  W  220


661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E  V  F  T  N  M  L  L  N  V  V  G  F  L  L  P  L  S  V  I  240


721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T  F  C  T  M  Q  I  M  Q  V  L  R  N  N  E  M  Q  K  F  K  260


781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E  I  Q  T  E  R  R  A  T  V  L  V  L  V  L  L  L  F  I  280


841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I  C  W  L  P  F  Q  I  S  T  F  L  D  T  L  H  R  L  G  I  300
```

Figure 31B

```
 901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG  960
 301 L   S   S   Q   D   E   R   I   I   D   V   I   T   Q   I   A   S   F   M   320


 961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A   Y   S   N   S   C   L   N   P   L   V   Y   V   I   V   G   K   R   F   R   340


1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG AGGGCTGCAG GTCAGAACCC 1080
 341 K   K   S   W   E   V   Y   Q   G   V   C   Q   K   E   G   C   R   S   E   P   360


1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I   Q   M   E   N   S   M   G   T   L   R   T   S   I   S   V   E   R   Q   I   380


1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H   K   L   Q   D   W   A   G   S   R   Q   *                          391


1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260


1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320


1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380


1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440


1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500


1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560


1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620


1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680


1681 GGTCCCTGAT AACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740


1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800


1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860


1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920


1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980


1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040
```

Figure 31C

```
2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100

2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160

2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220

2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280

2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340

2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400

2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460

2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520

2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580

2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640

2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700

2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760

2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820

2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880

2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940

2941 GAGGGCTAGA ACCTAGAAGG CTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000

3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060

3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120

3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180

3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240
```

Figure 31D

```
3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAAAA AAA 3733
```

Figure 32A

```
  1   CGCCCAACCCAAGTTCAAAGGCTGATAAGAGAGAAAATCTCATGAGGAGGTTTTAGTCTA   60

 61   GGGAAAGTCATTCAGTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTTCCTG   120
  1                                                  M   S   S   S   W     6

121   GCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACCATTGAGGAACAGGCCAA   180
  7    L   L   L   S   L   V   A   V   T   A   A   Q   S   T   I   E   E   Q   A   K    26

181   GACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTCTATCAAAGTTCACTTGC   240
 27    T   F   L   D   K   F   N   H   E   A   E   D   L   F   Y   Q   S   S   L   A    46

241   TTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATGAATAATGCTGG   300
 47    S   W   N   Y   N   T   N   I   T   E   E   N   V   Q   N   M   N   N   A   G    66

301   GGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCCCAAATGTATCCACTACA   360
 67    D   K   W   S   A   F   L   K   E   Q   S   T   L   A   Q   M   Y   P   L   Q    86

361   AGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTC   420
 87    E   I   Q   N   L   T   V   K   L   Q   L   Q   A   L   Q   Q   N   G   S   S    106

421   AGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCAT   480
107    V   L   S   E   D   K   S   K   R   L   N   T   I   L   N   T   M   S   T   I    126

481   CTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAATGCTTATTACTTGAACC   540
127    Y   S   T   G   K   V   C   N   P   D   N   P   Q   E   C   L   L   L   E   P    146

541   AGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAGAGGCTCTGGGCTTGGGA   600
147    G   L   N   E   I   M   A   N   S   L   D   Y   N   E   R   L   W   A   W   E    166

601   AAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTT   660
167    S   W   R   S   E   V   G   K   Q   L   R   P   L   Y   E   E   Y   V   V   L    186

661   GAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGA   720
187    K   N   E   M   A   R   A   N   H   Y   E   D   Y   G   D   Y   W   R   G   D    206

721   CTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGCCAGTTGATTGAAGATGT   780
207    Y   E   V   N   G   V   D   G   Y   D   Y   S   R   G   Q   L   I   E   D   V    226

781   GGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTTCATGCCTATGTGAGGGC   840
227    E   H   T   F   E   E   I   K   P   L   Y   E   H   L   H   A   Y   V   R   A    246

841   AAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCATTT   900
247    K   L   M   N   A   Y   P   S   Y   I   S   P   I   G   C   L   P   A   H   L    266
```

Figure 32B

```
 901   GCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTTCCCTTTGG    960
 267    L  G  D  M  W  G  R  F  W  T  N  L  Y  S  L  T  V  P  F  G     286


 961   ACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAG   1020
 287    Q  K  P  N  I  D  V  T  D  A  M  V  D  Q  A  W  D  A  Q  R    306


1021   AATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTTCCTAATATGACTCAAGG   1080
 307    I  F  K  E  A  E  K  F  F  V  S  V  G  L  P  N  M  T  Q  G    326


1081   ATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAGAAAGCAGTCTGCCATCC   1140
 327    F  W  E  N  S  M  L  T  D  P  G  N  V  Q  K  A  V  C  H  P    346


1141   CACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAT   1200
 347    T  A  W  D  L  G  K  G  D  F  R  I  L  M  C  T  K  V  T  M    366


1201   GGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGC   1260
 367    D  D  F  L  T  A  H  H  E  M  G  H  I  Q  Y  D  M  A  Y  A    386


1261   TGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGGA   1320
 387    A  Q  P  F  L  L  R  N  G  A  N  E  G  F  H  E  A  V  G  E    406


1321   AATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCCATTGGTCTTCTGTCACC   1380
 407    I  M  S  L  S  A  A  T  P  K  H  L  K  S  I  G  L  L  S  P    426


1381   CGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTCAAACAAGCACTCACGAT   1440
 427    D  F  Q  E  D  N  E  T  E  I  N  F  L  L  K  Q  A  L  T  I    446


1441   TGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGG   1500
 447    V  G  T  L  P  F  T  Y  M  L  E  K  W  R  W  M  V  F  K  G    466


1501   GGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATGAAGCGAGAGATAGTTGG   1560
 467    E  I  P  K  D  Q  W  M  K  K  W  W  E  M  K  R  E  I  V  G    486


1561   GGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCCGCATCTCTGTTCCATGT   1620
 487    V  V  E  P  V  P  H  D  E  T  Y  C  D  P  A  S  L  F  H  V    506


1621   TTCTAATGATTACTCATTCATTCGATATTACACAAGGACCCTTTACCAATTCCAGTTTCA   1680
 507    S  N  D  Y  S  F  I  R  Y  Y  T  R  T  L  Y  Q  F  Q  F  Q    526


1681   AGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCACAAATGTGACATCTCAAA   1740
 527    E  A  L  C  Q  A  A  K  H  E  G  P  L  H  K  C  D  I  S  N    546
```

Figure 32C

```
1741  CTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCCTG  1800
547    S   T   E   A   G   Q   K   L   F   N   M   L   R   L   G   K   S   E   P   W    566


1801  GACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA  1860
567    T   L   A   L   E   N   V   V   G   A   K   N   M   N   V   R   P   L   L   N    586


1861  CTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGGATG  1920
587    Y   F   E   P   L   F   T   W   L   K   D   Q   N   K   N   S   F   V   G   W    606


1921  GAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATC  1980
607    S   T   D   W   S   P   Y   A   D   Q   S   I   K   V   R   I   S   L   K   S    626


1981  AGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC  2040
627    A   L   G   D   K   A   Y   E   W   N   D   N   E   M   Y   L   F   R   S   S    646


2041  TGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGG  2100
647    V   A   Y   A   M   R   Q   Y   F   L   K   V   K   N   Q   M   I   L   F   G    666


2101  GGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCAC  2160
667    E   E   D   V   R   V   A   N   L   K   P   R   I   S   F   N   F   F   V   T    686


2161  TGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGAT  2220
687    A   P   K   N   V   S   D   I   I   P   R   T   E   V   E   K   A   I   R   M    706


2221  GTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGG  2280
707    S   R   S   R   I   N   D   A   F   R   L   N   D   N   S   L   E   F   L   G    726


2281  GATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTT  2340
727    I   Q   P   T   L   G   P   P   N   Q   P   P   V   S   I   W   L   I   V   F    746


2341  TGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAG  2400
747    G   V   V   M   G   V   I   V   V   G   I   V   I   L   I   F   T   G   I   R    766


2401  AGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGATAT  2460
767    D   R   K   K   K   N   K   A   R   S   G   E   N   P   Y   A   S   I   D   I    786


2461  TAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGATGTTCAGACCTCCTTTTA  2520
787    S   K   G   E   N   N   P   G   F   Q   N   T   D   D   V   Q   T   S   F   *    806


2521  GAAAAATCTATGTTTTTCCTCTTGAGGTGATTTTGTTGTATGTAAATGTTAATTTCATGG  2580


2581  TATAGAAAATATAAGATGATAAAGATATCATTAAATGTCAAAACTATGACTCTGTTCAGA  2640
```

Figure 32D

```
2641  AAAAAAATTGTCCAAAGACAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTC  2700

2701  AGTATTTATTTCTGTCTCTGGATTTGACTTCTGTTCTGTTTCTTAATAAGGATTTTGTAT  2760

2761  TAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTTCAGGGATAATCTAAAT  2820

2821  GTAAATGTCTGTTGAATTTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTTG  2880

2881  GATCTTGTATGGAATATGGATGGATCACTTGTAAGGACAGTGCCTGGGAACTGGTGTAGC  2940

2941  TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTTCATTTAATCCATTGTCAAGGATGA  3000

3001  CATGCTTTCTTCACAGTAACTCAGTTCAAGTACTATGGTGATTTGCCTACAGTGATGTTT  3060

3061  GGAATCGATCATGCTTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATCCAGGGAACAG  3120

3121  GTAGAGGACATTGCTTTTTCACTTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA  3180

3181  AACTAGAGCCAGGGGCCTCCGTGAACTCCCAGAGCATGCCTGATAGAAACTCATTTCTAC  3240

3241  TGTTCTCTAACTGTGGAGTGAATGGAAATTCCAACTGTATGTTCACCCTCTGAAGTGGGT  3300

3301  ACCCAGTCTCTTAAATCTTTTGTATTTGCTCACAGTGTTTGAGCAGTGCTGAGCACAAAG  3360

3361  CAGACACTCAATAAATGCTAGATTTACACACTCAAAAAAAAAAAA  3405
```

Figure 33A

```
  1  ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC  60
  1   M   H   L   I   D   Y   L   L   L   L   L   V   G   L   L   A   L   S   H   G   20


 61  CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG  120
 21   Q   L   H   V   E   H   D   G   E   S   C   S   N   S   S   H   Q   Q   I   L   40


121  GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC  180
 41   E   T   G   E   G   S   P   S   L   K   I   A   P   A   N   A   D   F   A   F   60


181  CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG  240
 61   R   F   Y   Y   L   I   A   S   E   T   P   G   K   N   I   F   F   S   P   L   80


241  AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG  300
 81   S   I   S   A   A   Y   A   M   L   S   L   G   A   C   S   H   S   R   S   Q   100


301  ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC  360
101   I   L   E   G   L   G   F   N   L   T   E   L   S   E   S   D   V   H   R   G   120


361  TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC  420
121   F   Q   H   L   L   H   T   L   N   L   P   G   H   G   L   E   T   R   V   G   140


421  AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG  480
141   S   A   L   F   L   S   H   N   L   K   F   L   A   K   F   L   N   D   T   M   160


481  GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG  540
161   A   V   Y   E   A   K   L   F   H   T   N   F   Y   D   T   V   G   T   I   Q   180


541  CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGTGAG  600
181   L   I   N   D   H   V   K   K   E   T   R   G   K   I   V   D   L   V   S   E   200


601  CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG  660
201   L   K   K   D   V   L   M   V   L   V   N   Y   I   Y   F   K   A   L   W   E   220


661  AAACCATTCATTTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA  720
221   K   P   F   I   S   S   R   T   T   P   K   D   F   Y   V   D   E   N   T   T   240


721  GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC  780
241   V   R   V   P   M   M   L   Q   D   Q   E   H   H   W   Y   L   H   D   R   Y   260


781  TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC  840
261   L   P   C   S   V   L   R   M   D   Y   K   G   D   A   T   V   F   F   I   L   280
```

Figure 33B

```
 841  CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG   900
 281   P   N   Q   G   K   M   R   E   I   E   E   V   L   T   P   E   M   L   M   R    300


 901  TGGAACAACTTGTTGCGGAAGAGGAATTTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG   960
 301   W   N   N   L   L   R   K   R   N   F   Y   K   K   L   E   L   H   L   P   K    320


 961  TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT  1020
 321   F   S   I   S   G   S   Y   V   L   D   Q   I   L   P   R   L   G   F   T   D    340


1021  CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC  1080
 341   L   F   S   K   W   A   D   L   S   G   I   T   K   Q   Q   K   L   E   A   S    360


1081  AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC  1140
 361   K   S   F   H   K   A   T   L   D   V   D   E   A   G   T   E   A   A   A   A    380


1141  ACCACGTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC  1200
 381   T   T   F   A   I   K   F   F   S   A   Q   T   N   R   H   I   L   R   F   N    400


1201  CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCCTCTTTCTGGGCAAG  1260
 401   R   P   F   L   V   V   I   F   S   T   S   T   Q   S   V   L   F   L   G   K    420


1261  GTCGTCGACCCCACGAAACCATAG  1284
 421   V   V   D   P   T   K   P   *    428
```

Figure 34A

```
  1  ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC   60
  1   M   H   L   I   D   Y   L   L   L   L   L   V   G   L   L   A   L   S   H   G    20


 61  CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG   120
 21   Q   L   H   V   E   H   D   G   E   S   C   S   N   S   S   H   Q   Q   I   L    40


121  GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC   180
 41   E   T   G   E   G   S   P   S   L   K   I   A   P   A   N   A   D   F   A   F    60


181  CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG   240
 61   R   F   Y   Y   L   I   A   S   E   T   P   G   K   N   I   F   F   S   P   L    80


241  AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG   300
 81   S   I   S   A   A   Y   A   M   L   S   L   G   A   C   S   H   S   R   S   Q   100


301  ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC   360
101   I   L   E   G   L   G   F   N   L   T   E   L   S   E   S   D   V   H   R   G   120


361  TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC   420
121   F   Q   H   L   L   H   T   L   N   L   P   G   H   G   L   E   T   R   V   G   140


421  AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG   480
141   S   A   L   F   L   S   H   N   L   K   F   L   A   K   F   L   N   D   T   M   160


481  GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG   540
161   A   V   Y   E   A   K   L   F   H   T   N   F   Y   D   T   V   G   T   I   Q   180


541  CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGTGAG   600
181   L   I   N   D   H   V   K   K   E   T   R   G   K   I   V   D   L   V   S   E   200


601  CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG   660
201   L   K   K   D   V   L   M   V   L   V   N   Y   I   Y   F   K   A   L   W   E   220


661  AAACCATTCATTTCCTCAAGGACCACTCCCAAAGACTTTTATGTTGATGAGAACACAACA   720
221   K   P   F   I   S   S   R   T   T   P   K   D   F   Y   V   D   E   N   T   T   240


721  GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC   780
241   V   R   V   P   M   M   L   Q   D   Q   E   H   H   W   Y   L   H   D   R   Y   260


781  TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC   840
261   L   P   C   S   V   L   R   M   D   Y   K   G   D   A   T   V   F   F   I   L   280
```

Figure 34B

```
 841  CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG   900
 281   P   N   Q   G   K   M   R   E   I   E   E   V   L   T   P   E   M   L   M   R    300


 901  TGGAACAACTTGTTGCGGAAGAGGAATTTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG   960
 301   W   N   N   L   L   R   K   R   N   F   Y   K   K   L   E   L   H   L   P   K    320


 961  TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT  1020
 321   F   S   I   S   G   S   Y   V   L   D   Q   I   L   P   R   L   G   F   T   D    340


1021  CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC  1080
 341   L   F   S   K   W   A   D   L   S   G   I   T   K   Q   Q   K   L   E   A   S    360


1081  AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC  1140
 361   K   S   F   H   K   A   T   L   D   V   D   E   A   G   T   E   A   A   A   A    380


1141  ACCACGTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC  1200
 381   T   T   F   A   I   K   F   F   S   A   Q   T   N   R   H   I   L   R   F   N    400


1201  CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCCTCTTTCTGGGCAAG  1260
 401   R   P   F   L   V   V   I   F   S   T   S   T   Q   S   V   L   F   L   G   K    420


1261  GTCGTCGACCCCACGAAACCATAG    1284
 421   V   V   D   P   T   K   P   *     428
```

Figure 35A

```
  1  ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC   60
  1   M   H   L   I   D   Y   L   L   L   L   L   V   G   L   L   A   L   S   H   G    20


 61  CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG  120
 21   Q   L   H   V   E   H   D   G   E   S   C   S   N   S   S   H   Q   Q   I   L    40


121  GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC  180
 41   E   T   G   E   G   S   P   S   L   K   I   A   P   A   N   A   D   F   A   F    60


181  CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG  240
 61   R   F   Y   Y   L   I   A   S   E   T   P   G   K   N   I   F   F   S   P   L    80


241  AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG  300
 81   S   I   S   A   A   Y   A   M   L   S   L   G   A   C   S   H   S   R   S   Q   100


301  ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC  360
101   I   L   E   G   L   G   F   N   L   T   E   L   S   E   S   D   V   H   R   G   120


361  TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC  420
121   F   Q   H   L   L   H   T   L   N   L   P   G   H   G   L   E   T   R   V   G   140


421  AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG  480
141   S   A   L   F   L   S   H   N   L   K   F   L   A   K   F   L   N   D   T   M   160


481  GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG  540
161   A   V   Y   E   A   K   L   F   H   T   N   F   Y   D   T   V   G   T   I   Q   180


541  CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGCGAG  600
181   L   I   N   D   H   V   K   K   E   T   R   G   K   I   V   D   L   V   S   E   200


601  CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG  660
201   L   K   K   D   V   L   M   V   L   V   N   Y   I   Y   F   K   A   L   W   E   220


661  AAACCATTCATTTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA  720
221   K   P   F   I   S   S   R   T   T   P   K   D   F   Y   V   D   E   N   T   T   240


721  GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC  780
241   V   R   V   P   M   M   L   Q   D   Q   E   H   H   W   Y   L   H   D   R   Y   260


781  TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC  840
261   L   P   C   S   V   L   R   M   D   Y   K   G   D   A   T   V   F   F   I   L   280
```

Figure 35B

```
 841  CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG   900
 281   P   N   Q   G   K   M   R   E   I   E   E   V   L   T   P   E   M   L   M   R    300


 901  TGGAACAACTTGTTGCGGAAGAGGAATTTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG   960
 301   W   N   N   L   L   R   K   R   N   F   Y   K   K   L   E   L   H.  L   P   K    320


 961  TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT  1020
 321   F   S   I   S   G   S   Y   V   L   D   Q   I   L   P   R   L   G   F   T   D    340


1021  CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC  1080
 341   L   F   S   K   W   A   D   L   S   G   I   T   K   Q   Q   K   L   E   A   S    360


1081  AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC  1140
 361   K   S   F   H   K   A   T   L   D   V   D   E   A   G   T   E   A   A   A   A    380


1141  ACCACGTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC  1200
 381   T   T   F   A   I   K   F   F   S   A   Q   T   N   R   H   I   L   R   F   N    400


1201  CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCCTCTTTCTGGGCAAG  1260
 401   R   P   F   L   V   V   I   F   S   T   S   T   Q   S   V   L   F   L   G   K    420


1261  GTCGTCGACCCCACGAAACCATAG  1284
 421   V   V   D   P   T   K   P   *    428
```

Figure 36A

```
  1   ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC   60
  1    M   H   L   I   D   Y   L   L   L   L   L   V   G   L   L   A   L   S   H   G    20


 61   CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG   120
 21    Q   L   H   V   E   H   D   G   E   S   C   S   N   S   S   H   Q   Q   I   L    40


121   GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC   180
 41    E   T   G   E   G   S   P   S   L   K   I   A   P   A   N   A   D   F   A   F    60


181   CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG   240
 61    R   F   Y   Y   L   I   A   S   E   T   P   G   K   N   I   F   F   S   P   L    80


241   AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG   300
 81    S   I   S   A   A   Y   A   M   L   S   L   G   A   C   S   H   S   R   S   Q   100


301   ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC   360
101    I   L   E   G   L   G   F   N   L   T   E   L   S   E   S   D   V   H   R   G   120


361   TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC   420
121    F   Q   H   L   L   H   T   L   N   L   P   G   H   G   L   E   T   R   V   G   140


421   AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG   480
141    S   A   L   F   L   S   H   N   L   K   F   L   A   K   F   L   N   D   T   M   160


481   GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG   540
161    A   V   Y   E   A   K   L   F   H   T   N   F   Y   D   T   V   G   T   I   Q   180


541   CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGNGAG   600
181    L   I   N   D   H   V   K   K   E   T   R   G   K   I   V   D   L   V   S   E   200


601   CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG   660
201    L   K   K   D   V   L   M   V   L   V   N   Y   I   Y   F   K   A   L   W   E   220


661   AAACCATTCATTTCCTCAAGGACCACTCCCAAAGACTTNTATGTTGATGAGAACACAACA   720
221    K   P   F   I   S   S   R   T   T   P   K   D   F   Y   V   D   E   N   T   T   240


721   GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC   780
241    V   R   V   P   M   M   L   Q   D   Q   E   H   H   W   Y   L   H   D   R   Y   260


781   TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC   840
261    L   P   C   S   V   L   R   M   D   Y   K   G   D   A   T   V   F   F   I   L   280
```

Figure 36B

```
 841   CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG   900
 281   P   N   Q   G   K   M   R   E   I   E   E   V   L   T   P   E   M   L   M   R    300


 901   TGGAACAACTTGTTGCGGAAGAGGAATTTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG   960
 301   W   N   N   L   L   R   K   R   N   F   Y   K   K   L   E   L   H   L   P   K    320


 961   TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT   1020
 321   F   S   I   S   G   S   Y   V   L   D   Q   I   L   P   R   L   G   F   T   D    340


1021   CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC   1080
 341   L   F   S   K   W   A   D   L   S   G   I   T   K   Q   Q   K   L   E   A   S    360


1081   AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC   1140
 361   K   S   F   H   K   A   T   L   D   V   D   E   A   G   T   E   A   A   A   A    380


1141   ACCACGTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC   1200
 381   T   T   F   A   I   K   F   F   S   A   Q   T   N   R   H   I   L   R   F   N    400


1201   CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCCTCTTTCTGGGCAAG   1260
 401   R   P   F   L   V   V   I   F   S   T   S   T   Q   S   V   L   F   L   G   K    420


1261   GTCGTCGACCCCACGAAACCATAG   1284
 421   V   V   D   P   T   K   P   *    428
```

Figure 37A

```
  1  CGCCCAACCCAAGTTCAAAGGCTGATAAGAGAGAAAATCTCATGAGGAGGTTTTAGTCTA    60

 61  GGGAAAGTCATTCAGTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTTCCTG   120
  1                                                    M   S   S   S   W     6

121  GCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACCATTGAGGAACAGGCCAA   180
  7   L   L   L   S   L   V   A   V   T   A   A   Q   S   T   I   E   E   Q   A   K    26

181  GACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTCTATCAAAGTTCACTTGC   240
 27   T   F   L   D   K   F   N   H   E   A   E   D   L   F   Y   Q   S   S   L   A    46

241  TTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATGAATAATGCTGG   300
 47   S   W   N   Y   N   T   N   I   T   E   E   N   V   Q   N   M   N   N   A   G    66

301  GGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCCCAAATGTATCCACTACA   360
 67   D   K   W   S   A   F   L   K   E   Q   S   T   L   A   Q   M   Y   P   L   Q    86

361  AGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTC   420
 87   E   I   Q   N   L   T   V   K   L   Q   L   Q   A   L   Q   Q   N   G   S   S    106

421  AGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCAT   480
107   V   L   S   E   D   K   S   K   R   L   N   T   I   L   N   T   M   S   T   I    126

481  CTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAATGCTTATTACTTGAACC   540
127   Y   S   T   G   K   V   C   N   P   D   N   P   Q   E   C   L   L   L   E   P    146

541  AGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAGAGGCTCTGGGCTTGGGA   600
147   G   L   N   E   I   M   A   N   S   L   D   Y   N   E   R   L   W   A   W   E    166

601  AAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTT   660
167   S   W   R   S   E   V   G   K   Q   L   R   P   L   Y   E   E   Y   V   V   L    186

661  GAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGA   720
187   K   N   E   M   A   R   A   N   H   Y   E   D   Y   G   D   Y   W   R   G   D    206

721  CTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGCCAGTTGATTGAAGATGT   780
207   Y   E   V   N   G   V   D   G   Y   D   Y   S   R   G   Q   L   I   E   D   V    226

781  GGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTTCATGCCTATGTGAGGGC   840
227   E   H   T   F   E   E   I   K   P   L   Y   E   H   L   H   A   Y   V   R   A    246

841  AAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCATTT   900
247   K   L   M   N   A   Y   P   S   Y   I   S   P   I   G   C   L   P   A   H   L    266
```

Figure 37B

```
901   GCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTTCCCTTTGG   960
267    L   G   D   M   W   G   R   F   W   T   N   L   Y   S   L   T   V   P   F   G    286


961   ACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAG   1020
287    Q   K   P   N   I   D   V   T   D   A   M   V   D   Q   A   W   D   A   Q   R    306


1021  AATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTTCCTAATATGACTCAAGG   1080
307    I   F   K   E   A   E   K   F   F   V   S   V   G   L   P   N   M   T   Q   G    326


1081  ATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAGAAAGCAGTCTGCCATCC   1140
327    F   W   E   N   S   M   L   T   D   P   G   N   V   Q   K   A   V   C   H   P    346


1141  CACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAT   1200
347    T   A   W   D   L   G   K   G   D   F   R   I   L   M   C   T   K   V   T   M    366


1201  GGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGC   1260
367    D   D   F   L   T   A   H   H   E   M   G   H   I   Q   Y   D   M   A   Y   A    386


1261  TGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGGA   1320
387    A   Q   P   F   L   L   R   N   G   A   N   E   G   F   H   E   A   V   G   E    406


1321  AATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCCATTGGTCTTCTGTCACC   1380
407    I   M   S   L   S   A   A   T   P   K   H   L   K   S   I   G   L   L   S   P    426


1381  CGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTCAAACAAGCACTCACGAT   1440
427    D   F   Q   E   D   N   E   T   E   I   N   F   L   L   K   Q   A   L   T   I    446


1441  TGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGG   1500
447    V   G   T   L   P   F   T   Y   M   L   E   K   W   R   W   M   V   F   K   G    466


1501  GGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATGAAGCGAGAGATAGTTGG   1560
467    E   I   P   K   D   Q   W   M   K   K   W   W   E   M   K   R   E   I   V   G    486


1561  GGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCCGCATCTCTGTTCCATGT   1620
487    V   V   E   P   V   P   H   D   E   T   Y   C   D   P   A   S   L   F   H   V    506


1621  TTCTAATGATTACTCATTCATTCGATATTACACAAGGACCCTTTACCAATTCCAGTTTCA   1680
507    S   N   D   Y   S   F   I   R   Y   Y   T   R   T   L   Y   Q   F   Q   F   Q    526


1681  AGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCACAAATGTGACATCTCAAA   1740
527    E   A   L   C   Q   A   A   K   H   E   G   P   L   H   K   C   D   I   S   N    546
```

Figure 37C

```
1741  CTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCCTG  1800
547    S   T   E   A   G   Q   K   L   F   N   M   L   R   L   G   K   S   E   P   W   566


1801  GACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA  1860
567    T   L   A   L   E   N   V   V   G   A   K   N   M   N   V   R   P   L   L   N   586


1861  CTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGGATG  1920
587    Y   F   E   P   L   F   T   W   L   K   D   Q   N   K   N   S   F   V   G   W   606


1921  GAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATC  1980
607    S   T   D   W   S   P   Y   A   D   Q   S   I   K   V   R   I   S   L   K   S   626


1981  AGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC  2040
627    A   L   G   D   K   A   Y   E   W   N   D   N   E   M   Y   L   F   R   S   S   646


2041  TGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGG  2100
647    V   A   Y   A   M   R   Q   Y   F   L   K   V   K   N   Q   M   I   L   F   G   666


2101  GGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCAC  2160
667    E   E   D   V   R   V   A   N   L   K   P   R   I   S   F   N   F   F   V   T   686


2161  TGCACCTAAAAACGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGAT  2220
687    A   P   K   N   V   S   D   I   I   P   R   T   E   V   E   K   A   I   R   M   706


2221  GTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGG  2280
707    S   R   S   R   I   N   D   A   F   R   L   N   D   N   S   L   E   F   L   G   726


2281  GATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTT  2340
727    I   Q   P   T   L   G   P   P   N   Q   P   P   V   S   I   W   L   I   V   F   746


2341  TGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAG  2400
747    G   V   V   M   G   V   I   V   V   G   I   V   I   L   I   F   T   G   I   R   766


2401  AGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGATAT  2460
767    D   R   K   K   K   N   K   A   R   S   G   E   N   P   Y   A   S   I   D   I   786


2461  TAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGATGTTCAGACCTCCTTTTA  2520
787    S   K   G   E   N   N   P   G   F   Q   N   T   D   D   V   Q   T   S   F   *   806


2521  GAAAAATCTATGTTTTTCCTCTTGAGGTGATTTTGTTGTATGTAAATGTTAATTTCATGG  2580


2581  TATAGAAAATATAAGATGATAAAGATATCATTAAATGTCAAAACTATGACTCTGTTCAGA  2640
```

Figure 37D

```
2641  AAAAAAATTGTCCAAAGACAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTC   2700

2701  AGTATTTATTTCTGTCTCTGGATTTGACTTCTGTTCTGTTTCTTAATAAGGATTTTGTAT   2760

2761  TAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTTCAGGGATAATCTAAAT   2820

2821  GTAAATGTCTGTTGAATTTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTTG   2880

2881  GATCTTGTATGGAATATGGATGGATCACTTGTAAGGACAGTGCCTGGGAACTGGTGTAGC   2940

2941  TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTTCATTTAATCCATTGTCAAGGATGA   3000

3001  CATGCTTTCTTCACAGTAACTCAGTTCAAGTACTATGGTGATTTGCCTACAGTGATGTTT   3060

3061  GGAATCGATCATGCTTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATCCAGGGAACAG   3120

3121  GTAGAGGACATTGCTTTTTCACTTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA   3180

3181  AACTAGAGCCAGGGGCCTCCGTGAACTCCCAGAGCATGCCTGATAGAAACTCATTTCTAC   3240

3241  TGTTCTCTAACTGTGGAGTGAATGGAAATTCCAACTGTATGTTCACCCTCTGAAGTGGGT   3300

3301  ACCCAGTCTCTTAAATCTTTTGTATTTGCTCACAGTGTTTGAGCAGTGCTGAGCACAAAG   3360

3361  CAGACACTCAATAAATGCTAGATTTACACACTCAAAAAAAAAAAA   3405
```

Figure 38A

```
  1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTN GTGAGGNCTC CGTGCCCACC  60
  1 M  F  S  P  W  K  I  S  M  F  L  S  V  X  E  X  S  V  P  T   20

 61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
 21 T  A  S  F  S  A  D  M  L  N  V  T  L  Q  G  P  T  L  N  G   40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T  F  A  Q  S  K  C  P  Q  V  E  W  L  G  W  L  N  T  I  Q   60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
 61 P  P  F  L  W  V  L  F  V  L  A  T  L  E  N  I  F  V  L  S   80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V  F  C  L  H  K  S  S  C  T  V  A  E  I  Y  L  G  N  L  A  100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A  A  D  L  I  L  A  C  G  L  P  F  W  A  I  T  I  S  N  N  120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F  D  W  L  F  G  E  T  L  C  R  V  V  N  A  I  I  S  M  N  140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L  Y  S  S  I  C  F  L  M  L  V  S  I  D  R  Y  L  A  L  V  160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K  T  M  S  M  G  R  M  R  G  V  R  W  A  K  L  Y  S  L  V  180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
181 I  W  G  C  T  L  L  L  S  S  P  M  L  V  F  R  T  M  K  E  200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y  S  D  E  G  H  N  V  T  A  C  V  I  S  Y  P  S  L  I  W  220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E  V  F  T  N  M  L  L  N  V  V  G  F  L  L  P  L  S  V  I  240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T  F  C  T  M  Q  I  M  Q  V  L  R  N  N  E  M  Q  K  F  K  260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E  I  Q  T  E  R  R  A  T  V  L  V  L  V  L  L  L  F  I  280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I  C  W  L  P  F  Q  I  S  T  F  L  D  T  L  H  R  L  G  I  300
```

Figure 38B

```
 901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GANGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L    S    S    C    Q    D    E    R    I    I    D    V    I    T    Q    I    A    S    F    M    320

 961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A    Y    S    N    S    C    L    N    P    L    V    Y    V    I    V    G    K    R    F    R    340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG NGGGCTGCAG GTCAGAACCC 1080
 341 K    K    S    W    E    V    Y    Q    G    V    C    Q    K    X    G    C    R    S    E    P    360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I    Q    M    E    N    S    M    G    T    L    R    T    S    I    S    V    E    R    Q    I    380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H    K    L    Q    D    W    A    G    S    R    Q    *                                    391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040
```

Figure 38C

```
2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100

2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160

2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220

2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280

2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340

2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400

2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460

2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520

2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580

2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640

2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700

2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760

2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820

2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880

2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940

2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000

3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060

3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120

3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180

3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTTAAA GCAAAGCGT GAAAAAAAAG 3240
```

Figure 38D

```
3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAAA AAA 3733
```

Figure 39
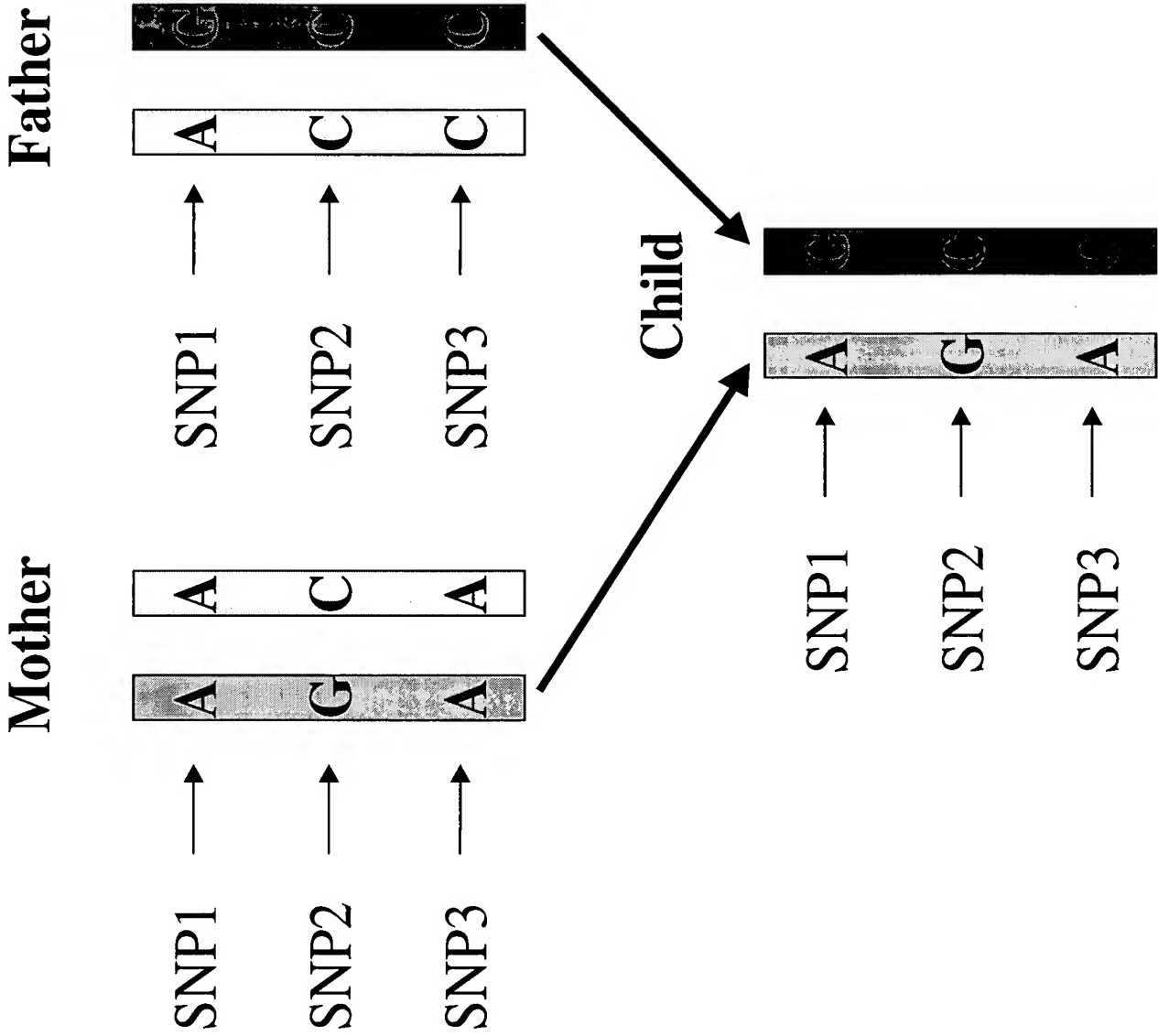
SNP1 (A/G) →

SNP2 (G/C) →

SNP3 (C/A) →

Figure 40

Figure 41A

```
  1 CACCCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60


 61 TGCCCACCCT GGCTCCCAAA ACCCTCCAAA ACAAAGACC AGAAAAGCAC TCTCCACCCA 120


121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCCAGGAA 180


181 AGGCCTGAAG GAACAGGCCG GGGAAGGAGC CCTCCCTCTC TCCCTTGTCC CTCCATCCAC 240


241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
  1                       M   A   R   A   H   W   G   C   C   P   W   L  12


301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13  V   L   L   C   A   C   A   W   G   H   T   K   P   L   D   L   G   G   Q   D  32


361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33  V   R   N   C   S   T   N   P   P   Y   L   P   V   T   V   V   N   T   T   M  52


421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53  S   L   T   A   L   R   Q   Q   M   Q   T   Q   N   L   S   A   Y   I   I   P  72


481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCGTGGATT 540
 73  G   T   D   A   H   M   N   E   Y   I   G   Q   H   D   E   R   R   A   W   I  92


541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
 93  T   G   F   T   G   S   A   G   T   A   V   V   T   M   K   K   A   A   V   W 112


601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
113  T   D   S   R   Y   W   T   Q   A   E   R   Q   M   D   C   N   W   E   L   H 132


661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC TGCTGGAGGG 720
133  K   E   V   G   T   T   P   I   V   T   W   L   L   T   E   I   P   A   G   G 152


721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
153  R   V   G   F   D   P   F   L   L   S   I   D   T   W   E   S   Y   D   L   A 172


781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTGGA CCTGGTATGG 840
173  L   Q   G   S   N   R   Q   L   V   S   I   T   T   N   L   V   D   L   V   W 192


841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900
193  G   S   E   R   P   P   V   P   N   Q   P   I   Y   A   L   Q   E   A   F   T 212


901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
213  G   S   T   W   Q   E   K   V   S   G   V   R   S   Q   M   Q   K   H   Q   K 232
```

Figure 41B

```
 961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V   P   T   A  V   L   L   S   A   L   E   E   T   A  W   L   F   N   L   R   252


1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
 253 A   S   D   I   P   Y   N   P   F   F   Y  'S   Y   T   L   L   T   D   S   S   272


1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACTCC 1140
 273 I   R   L   F   A   N   K   S   R   F   S   S   E   T   L   S   Y   L   N   S   292


1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S   C   T   G   P   M   C   V   Q   I   E   D   Y   S   Q   V   R   D   S   I   312


1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q   A   Y   S   L   G   D   V   R   I   W   I   G   T   S   Y   T   M   Y   G   332


1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I   Y   E   M   I   P   R   E   K   L   V   T   D   T   Y   S   P   V   M   M   352


1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
 353 T   K   A   V   K   N   S   K   E   Q   A   L   L   K   A   S   H   V   R   D   372


1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
 373 A   V   A   V   I   R   Y   L   V   W   L   E   K   N   V   P   K   G   T   V   392


1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
 393 D   E   F   S   G   A   E   I   V   D   K   F   R   G   E   E   Q   F   S   S   412


1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
 413 G   P   S   F   E   T   I   S   A   S   G   L   N   A   A   L   A   H   Y   S   432


1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P   T   K   E   L   N   R   K   L   S   S   D   E   M   Y   L   L   D   S   G   452


1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
 453 G   Q   Y   W   D   G   T   T   D   I   T   R   T   V   H   W   G   T   P   S   472


1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A   F   Q   K   E   A   Y   T   R   V   L   I   G   N   I   D   L   S   R   L   492


1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
 493 I   F   P   A   A   T   S   G   R   M   V   E   A   F   A   R   R   A   L   W   512


1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
 513 D   A   G   L   N   Y   G   H   G   T   G   H   G   I   G   N   F   L   C   V   532
```

Figure 41C

```
1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533  H  E  W   P  V  G  F   Q  S  N   N  I  A  M   A  K  G    M  F  T  552


1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553  S  I  E   P  G  Y  Y   K  D  G    E  F  G  I   R  L  E    D  V  A  572


1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573  L  V  V   E  A  K  T   K  Y  P    G  E  L  P    D  L  V   V  S  F  592


2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCGAGCA TCTCCAGTAC 2100
 593  V  P  Y   D  R  N  L   I  D  V    S  L  L  S   P  E  H    L  Q  Y  612


2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613  L  N  R   Y  Y  Q  T   I  R  E    K  V  G  P    E  L  Q   R  R  Q  632


2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633  L  L  E   E  F  E  W   L  Q  Q    H  T  E  P    L  A  A   R  A  P  652


2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653  D  T  A   S  W  A  S   V  L  V    V  S  T  L    A  I  L   G  W  S  672


2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673  V  *                                                               673


2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400


2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460


2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520


2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580


2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640


2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700


2701 CCTGTCACCG CGTGTTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760


2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820


2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880


2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940
```

Figure 41D

```
2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000

3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTC GAGGAGCCCT TTGAACTTTC 3060

3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCCTTC 3120

3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAACTG AGCTTCAGAC 3180

3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240

3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300

3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360

3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420

3421 GCCTGTGG 3428
```

Figure 42A

```
  1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC  60
  1     M    A    S    S    W    P    P    L    E    L    Q    S    S    N    Q    S    Q    L   18


 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19     F    P    Q    N    A    T    A    C    D    N    A    P    E    A    W    D    L    L    H    R   38


121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39     V    L    P    T    F    I    I    S    I    C    F    F    G    L    L    G    N    L    F    V   58


181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59     L    L    V    F    L    L    P    R    R    Q    L    N    V    A    E    I    Y    L    A    N   78


241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79     L    A    A    S    D    L    V    F    V    L    G    L    P    F    W    A    E    N    I    W   98


301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99     N    Q    F    N    W    P    F    G    A    L    L    C    R    V    I    N    G    V    I    K  118


361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119     A    N    L    F    I    S    I    F    L    V    V    A    I    S    Q    D    R    Y    R    V  138


421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
139     L    V    H    P    M    A    S    G    R    Q    Q    R    R    R    Q    A    R    V    T    C  158


481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159     V    L    I    W    V    V    G    G    L    L    S    I    P    T    F    L    L    R    S    I  178


541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179     Q    A    V    P    D    L    N    I    T    A    C    I    L    L    L    P    H    E    A    W  198


601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199     H    F    A    R    I    V    E    L    N    I    L    G    F    L    L    P    L    A    A    I  218


661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219     V    F    F    N    Y    H    I    L    A    S    L    R    T    R    E    E    V    S    R    T  238


721 AGAGTGCAGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239     R    V    Q    G    P    K    D    S    K    T    T    A    L    I    L    T    L    V    V    A  258


781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259     F    L    V    C    W    A    P    Y    H    F    F    A    F    L    E    F    L    F    Q    V  278


841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279     Q    A    V    R    G    C    F    W    E    D    F    I    D    L    G    L    Q    L    A    N  298
```

Figure 42B

```
901  TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC  960
299  F    F    A    F    T    N    S    S    L    N    P    V    I    Y    V    F    V    G    R    L   318


961  TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319  F    R    T    K    V    W    E    L    Y    K    Q    C    T    P    K    S    L    A    P    I   338


1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339  S    S    S    H    R    K    E    I    F    Q    L    F    W    R    N    *                       353


1081 CC 1082
```

Figure 43A

```
  1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGCCTC CGTGCCCACC 60
  1 M  F  S  P  W  K  I  S  M  F  L  S  V  R  E  A  S  V  P  T  20
```

```
 61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
 21 T  A  S  F  S  A  D  M  L  N  V  T  L  Q  G  P  T  L  N  G  40
```

```
121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T  F  A  Q  S  K  C  P  Q  V  E  W  L  G  W  L  N  T  I  Q  60
```

```
181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
 61 P  P  F  L  W  V  L  F  V  L  A  T  L  E  N  I  F  V  L  S  80
```

```
241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V  F  C  L  H  K  S  S  C  T  V  A  E  I  Y  L  G  N  L  A  100
```

```
301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A  A  D  L  I  L  A  C  G  L  P  F  W  A  I  T  I  S  N  N  120
```

```
361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F  D  W  L  F  G  E  T  L  C  R  V  V  N  A  I  I  S  M  N  140
```

```
421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L  Y  S  S  I  C  F  L  M  L  V  S  I  D  R  Y  L  A  L  V  160
```

```
481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K  T  M  S  M  G  R  M  R  G  V  R  W  A  K  L  Y  S  L  V  180
```

```
541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600
181 I  W  G  C  T  L  L  L  S  S  P  M  L  V  F  R  T  M  K  E  200
```

```
601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y  S  D  E  G  H  N  V  T  A  C  V  I  S  Y  P  S  L  I  W  220
```

```
661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E  V  F  T  N  M  L  L  N  V  V  G  F  L  L  P  L  S  V  I  240
```

```
721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T  F  C  T  M  Q  I  M  Q  V  L  R  N  N  E  M  Q  K  F  K  260
```

```
781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E  I  Q  T  E  R  R  A  T  V  L  V  L  V  V  L  L  F  I  280
```

```
841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I  C  W  L  P  F  Q  I  S  T  F  L  D  T  L  H  R  L  G  I  300
```

Figure 43B

```
901  CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
301  L   S   S   C   Q   D   E   R   I   I   D   V   I   T   Q   I   A   S   F   M  320


961  GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
321  A   Y   S   N   S   C   L   N   P   L   V   Y   V   I   V   G   K   R   F   R  340


1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
341  K   K   S   W   E   V   Y   Q   G   V   C   Q   K   G   G   C   R   S   E   P  360


1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
361  I   Q   M   E   N   S   M   G   T   L   R   T   S   I   S   V   E   R   Q   I  380


1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
381  H   K   L   Q   D   W   A   G   S   R   Q   *                               391


1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260


1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320


1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380


1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440


1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500


1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560


1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620


1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680


1681 GGTCCCTGAT AACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740


1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800


1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860


1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920


1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980


1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040
```

Figure 43C

```
2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100

2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160

2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220

2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280

2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340

2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400

2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460

2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520

2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580

2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640

2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700

2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760

2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820

2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880

2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940

2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000

3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060

3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120

3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180

3181 GAGCCCATAA ATCCTGACCA ATCCAACTCT GAATTTTAAA GCAAAGCGT GAAAAAAAAG 3240
```

Figure 43D

```
3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300

3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360

3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420

3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480

3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540

3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600

3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660

3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720

3721 AAAAAAAAAA AAA 3733
```

Figure 44A

```
  1  ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC   60
  1  M   H   L   I   D   Y   L   L   L   L   L   V   G   L   L   A   L   S   H   G    20

 61  CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG  120
 21  Q   L   H   V   E   H   D   G   E   S   C   S   N   S   S   H   Q   Q   I   L    40

121  GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC  180
 41  E   T   G   E   G   S   P   S   L   K   I   A   P   A   N   A   D   F   A   F    60

181  CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG  240
 61  R   F   Y   Y   L   I   A   S   E   T   P   G   K   N   I   F   F   S   P   L    80

241  AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG  300
 81  S   I   S   A   A   Y   A   M   L   S   L   G   A   C   S   H   S   R   S   Q   100

301  ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC  360
101  I   L   E   G   L   G   F   N   L   T   E   L   S   E   S   D   V   H   R   G   120

361  TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC  420
121  F   Q   H   L   L   H   T   L   N   L   P   G   H   G   L   E   T   R   V   G   140

421  AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG  480
141  S   A   L   F   L   S   H   N   L   K   F   L   A   K   F   L   N   D   T   M   160

481  GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG  540
161  A   V   Y   E   A   K   L   F   H   T   N   F   Y   D   T   V   G   T   I   Q   180

541  CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGTGAG  600
181  L   I   N   D   H   V   K   K   E   T   R   G   K   I   V   D   L   V   S   E   200

601  CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG  660
201  L   K   K   D   V   L   M   V   L   V   N   Y   I   Y   F   K   A   L   W   E   220

661  AAACCATTCATTTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA  720
221  K   P   F   I   S   S   R   T   T   P   K   D   F   Y   V   D   E   N   T   T   240

721  GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC  780
241  V   R   V   P   M   M   L   Q   D   Q   E   H   H   W   Y   L   H   D   R   Y   260

781  TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC  840
261  L   P   C   S   V   L   R   M   D   Y   K   G   D   A   T   V   F   F   I   L   280
```

Figure 44B

```
 841   CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG    900
 281    P  N  Q  G  K  M  R  E  I  E  E  V  L  T  P  E  M  L  M  R     300


 901   TGGAACAACTTGTTGCGGAAGAGGAATTTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG    960
 301    W  N  N  L  L  R  K  R  N  F ·Y  K  K  L  E  L  H  L  P  K     320


 961   TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT   1020
 321    F  S  I  S  G  S  Y  V  L  D  Q  I  L  P  R  L  G  F  T  D     340


1021   CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC   1080
 341    L  F  S  K  W  A  D  L  S  G  I  T  K  Q  Q  K  L  E  A  S     360


1081   AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC   1140
 361    K  S  F  H  K  A  T  L  D  V  D  E  A  G  T  E  A  A  A  A     380


1141   ACGACGTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC   1200
 381    T  T  F  A  I  K  F  F  S  A  Q  T  N  R  H  I  L  R  F  N     400


1201   CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCCTCTTTCTGGGCAAG   1260
 401    R  P  F  L  V  V  I  F  S  T  S  T  Q  S  V  L  F  L  G  K     420


1261   GTCGTCGACCCCACGAAACCATAG   1284
 421    V  V  D  P  T  K  P  *     428
```

Figure 45A

```
  1  ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC   60
  1  M   H   L   I   D   Y   L   L   L   L   L   V   G   L   L   A   L   S   H   G    20


 61  CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG   120
 21  Q   L   H   V   E   H   D   G   E   S   C   S   N   S   S   H   Q   Q   I   L    40


121  GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC   180
 41  E   T   G   E   G   S   P   S   L   K   I   A   P   A   N   A   D   F   A   F    60


181  CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG   240
 61  R   F   Y   Y   L   I   A   S   E   T   P   G   K   N   I   F   F   S   P   L    80


241  AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG   300
 81  S   I   S   A   A   Y   A   M   L   S   L   G   A   C   S   H   S   R   S   Q   100


301  ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC   360
101  I   L   E   G   L   G   F   N   L   T   E   L   S   E   S   D   V   H   R   G   120


361  TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACaTGCGTGGGC   420
121  F   Q   H   L   L   H   T   L   N   L   P   G   H   G   L   E   T   C   V   G   140


421  AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG   480
141  S   A   L   F   L   S   H   N   L   K   F   L   A   K   F   L   N   D   T   M   160


481  GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG   540
161  A   V   Y   E   A   K   L   F   H   T   N   F   Y   D   T   V   G   T   I   Q   180


541  CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGTGAG   600
181  L   I   N   D   H   V   K   K   E   T   R   G   K   I   V   D   L   V   S   E   200


601  CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG   660
201  L   K   K   D   V   L   M   V   L   V   N   Y   I   Y   F   K   A   L   W   E   220


661  AAACCATTCATTTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA   720
221  K   P   F   I   S   S   R   T   T   P   K   D   F   Y   V   D   E   N   T   T   240


721  GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC   780
241  V   R   V   P   M   M   L   Q   D   Q   E   H   H   W   Y   L   H   D   R   Y   260


781  TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC   840
261  L   P   C   S   V   L   R   M   D   Y   K   G   D   A   T   V   F   F   I   L   280
```

Figure 45B

```
 841   CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG    900
 281   P   N   Q   G   K   M   R   E   I   E   E   V   L   T   P   E   M   L   M   R    300


 901   TGGAACAACTTGTTGCGGAAGAGGAATTTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG    960
 301   W   N   N   L   L   R   K   R   N   F   Y   K   K   L   E   L   H   L   P   K    320


 961   TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT   1020
 321   F   S   I   S   G   S   Y   V   L   D   Q   I   L   P   R   L   G   F   T   D    340


1021   CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC   1080
 341   L   F   S   K   W   A   D   L   S   G   I   T   K   Q   Q   K   L   E   A   S    360


1081   AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC   1140
 361   K   S   F   H   K   A   T   L   D   V   D   E   A   G   T   E   A   A   A   A    380


1141   ACCACGTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC   1200
 381   T   T   F   A   I   K   F   F   S   A   Q   T   N   R   H   I   L   R   F   N    400


1201   CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCCTCTTTCTGGGCAAG   1260
 401   R   P   F   L   V   V   I   F   S   T   S   T   Q   S   V   L   F   L   G   K    420


1261   GTCGTCGACCCCACGAAACCATAG    1284
 421   V   V   D   P   T   K   P   *        428
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Figure 46A

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  1 CACCCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60


 61 TGCCCACCCT GGCTCCCAAA ACCCTCCAAA ACAAAGACC  AGAAAGCAC  TCTCCACCCA 120


121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCCAGGAA 180


181 AGGCCTGAAG GAACAGGCCG GGGAAGGAGC CCTCCCTCTC TCCCTTGTCC CTCCATCCAC 240


241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
  1                      M   A   R   H   W   G   C   C   P   W   L   12


301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V   L   L   C   A   C   A   W   G   H   T   K   P   L   D   L   G   G   Q   D   32


361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V   R   N   C   S   T   N   P   P   Y   L   P   V   T   V   V   N   T   T   M   52


421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S   L   T   A   L   R   Q   Q   M   Q   T   Q   N   L   S   A   Y   I   I   P   72


481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCGTGGATT 540
 73 G   T   D   A   H   M   N   E   Y   I   G   Q   H   D   E   R   R   A   W   I   92


541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
 93 T   G   F   T   G   S   A   G   T   A   V   V   T   M   K   K   A   A   V   W   112


601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
113 T   D   S   R   Y   W   T   Q   A   E   R   Q   M   D   C   N   W   E   L   H   132


661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC NGCTGGAGGG 720
133 K   E   V   G   T   T   P   I   V   T   W   L   L   T   E   I   P   A   G   G   152


721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
153 R   V   G   F   D   P   F   L   L   S   I   D   T   W   E   S   Y   D   L   A   172


781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTGGA CCTGGTATGG 840
173 L   Q   G   S   N   R   Q   L   V   S   I   T   T   N   L   V   D   L   V   W   192


841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900
193 G   S   E   R   P   P   V   P   N   Q   P   I   Y   A   L   Q   E   A   F   T   212


901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
213 G   S   T   W   Q   E   K   V   S   G   V   R   S   Q   M   Q   K   H   Q   K   232
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Figure 46B

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 961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V  P  T  A  V  L  L  S  A  L  E  E  T  A  W  L  F  N  L  R  252


1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
 253 A  S  D  I  P  Y  N  P  F  F  Y  S  Y  T  L  L  T  D  S  S  272


1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACTCC 1140
 273 I  R  L  F  A  N  K  S  R  F  S  S  E  T  L  S  Y  L  N  S  292


1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
 293 S  C  T  G  P  M  C  V  Q  I  E  D  Y  S  Q  V  R  D  S  I  312


1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q  A  Y  S  L  G  D  V  R  I  W  I  G  T  S  Y  T  M  Y  G  332


1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I  Y  E  M  I  P  R  E  K  L  V  T  D  T  Y  S  P  V  M  M  352


1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
 353 T  K  A  V  K  N  S  K  E  Q  A  L  L  K  A  S  H  V  R  D  372


1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
 373 A  V  A  V  I  R  Y  L  V  W  L  E  K  N  V  P  K  G  T  V  392


1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
 393 D  E  F  S  G  A  E  I  V  D  K  F  R  G  E  E  Q  F  S  S  412


1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
 413 G  P  S  F  E  T  I  S  A  S  G  L  N  A  A  L  A  H  Y  S  432


1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P  T  K  E  L  N  R  K  L  S  S  D  E  M  Y  L  L  D  S  G  452


1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
 453 G  Q  Y  W  D  G  T  T  D  I  T  R  T  V  H  W  G  T  P  S  472


1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A  F  Q  K  E  A  Y  T  R  V  L  I  G  N  I  D  L  S  R  L  492


1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
 493 I  F  P  A  A  T  S  G  R  M  V  E  A  F  A  R  R  A  L  W  512


1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
 513 D  A  G  L  N  Y  G  H  G  T  G  H  G  I  G  N  F  L  C  V  532
```

Figure 46C

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1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H   E   W    P    V   G   F    Q   S   N    N   I   A   M    A   K   G    M   F   T    552


1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S   I   E    P    G   Y   Y    K   D   G    E   F   G   I    R   L   E    D   V   A    572


1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L   V   V    E   A   K   T    K   Y   P    G   E   L    P    D   L   V    V   S   F    592


2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCNGAGCA TCTCCAGTAC 2100
 593 V   P   Y    D   R   N   L    I   D   V    S   L   L    S    P   E   H    L   Q   Y    612


2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L   N   R   Y    Y   Q   T    I   R   E    K   V   G    P    E   L   Q    R   R   Q    632


2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L   L   E   E    F   E   W    L   Q   Q    H   T   E    P    L   A   A    R   A   P    652


2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D   T   A    S    W   A   S    V   L   V    V   S   T    L    A   I   L    G   W   S    672


2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V   *                                                                 673


2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400


2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460


2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520


2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580


2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640


2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700


2701 CCTGTCACCG CGTGTTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760


2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820


2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880


2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940
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Figure 46D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000

3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTC GAGGAGCCCT TTGAACTTTC 3060

3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCCTTC 3120

3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAACTG AGCTTCAGAC 3180

3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240

3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300

3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360

3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420

3421 GCCTGTGG 3428